

145891

STIC-Biotech/ChemLib

From: Bunner, Bridget
Sent: Wednesday, February 23, 2005 9:28 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/056,583:

Please search the following short, related amino acid sequences:

1. SEQ ID NO: 65
2. SEQ ID NO: 86
3. SEQ ID NO: 89
4. SEQ ID NO: 90
5. SEQ ID NO: 93
6. SEQ ID NO: 97

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STIC
FEB 23 2005
10:00 AM

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # 6 _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QSP _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 / Search time 76.6837 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583A-93

Perfect score: 74

Sequence: 1 EKPKEVAYKAAAPPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	5	ABP52299 HLA-DR2 m
2	69	93.2	15	5	ABP52291 HLA-DR2 m
3	69	93.2	15	5	ABP52297 HLA-DR2 m
4	68	91.9	15	5	ABP52305 HLA-DR2 m
5	64	86.5	15	5	ABP52300 HLA-DR2 m
6	63	85.1	15	5	ABP52290 HLA-DR2 m
7	63	85.1	15	5	ABP52292 HLA-DR2 m
8	63	85.1	15	5	ABP52304 HLA-DR2 m
9	61	82.4	17	5	ABP52303 HLA-DR2 m
10	58	78.4	781	8	ADN60395
11	58	78.4	781	8	ADN60395 B. lichen
12	58	78.4	781	8	ADN60519
13	57	77.0	17	5	ABP52302 HLA-DR2 m
14	53	71.6	15	5	ABP52271 HLA-DR2 m
15	53	71.6	15	5	ABP52289 HLA-DR2 m
16	53	71.6	15	5	ABP52298 HLA-DR2 m
17	53	71.6	17	5	ABP52294 HLA-DR2 m
18	53	71.6	17	5	ABP52296 HLA-DR2 m
19	53	71.6	19	5	ABP52295 HLA-DR2 m
20	49	66.2	15	5	ABP52293 HLA-DR2 m
21	49	66.2	15	5	ABP52301 HLA-DR2 m
22	48	64.9	299	4	ABP63276 Drosophila
23	48	64.9	299	4	ADN96704 Drosophila
24	47	63.5	15	5	ABP52270 HLA-DR2 m
25	47	63.5	15	5	ABP52272 HLA-DR2 m

26	44	59.5	362	3	AAg17822 Arabidops
27	44	59.5	364	3	AAg46637 Arabidops
28	44	59.5	461	3	AAg17821 Arabidops
29	44	59.5	462	3	AAg17820 Arabidops
30	44	59.5	463	3	AAg46636 Arabidops
31	44	59.5	464	3	AAg46635 Arabidops
32	44	59.5	572	4	ABP59072 Drosophila
33	43	58.1	15	5	ABP52263 HLA-DR2 m
34	43	58.1	428	8	ADN27881 Bacterial
35	42	56.8	306	4	AAU59347 Propionib
36	42	56.8	306	6	ABM55866 Propionib
37	42	56.8	312	2	AAW64153 Lettuce p
38	42	56.8	314	5	AAU95466 Lettuce p
39	42	56.8	444	4	ABG18307 Novel hum
40	42	56.8	774	4	ABG29304 Novel hum
41	42	56.8	791	8	ADQ26342 Chromobac
42	42	56.8	1402	2	AAW64150 Lettuce r
43	42	56.8	1402	5	AAU95463 Lettuce p
44	41	55.4	15	5	ABP52264 HLA-DR2 m
45	41	55.4	15	5	ABP52267 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52299 standard; peptide; 15 AA.
ID ABP52299 standard; peptide; 15 AA.
AC ABP52299;
XX
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:93.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200259143-A2.
XX
XX PD 01-AUG-2002.
XX
XX PF 24-JAN-2002; 2002WO-US002071.
XX
XX PR 24-JAN-2001; 2001US-0263569P.
XX
XX PA (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridakis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX PT New compositions comprising synthetic peptide in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX residues. The complex of the peptide with a major histocompatibility
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX immune response. (I) has antiinflammatory and neuroprotective activities,
XX and can be used as a MHC class II protein inhibitor. The compositions
XX comprising the peptide are useful for treating demyelinating diseases

CC such as asymptotic sclerostis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autocalcigen-specific HLA-DR2-restricted T cell clones. ABB52207 to
CC ABB52305 represent peptides used in the exemplification of the present
CC invention

SQ Sequence 15 AA;

Query Match	100.0%	Score 74	DB 5	Length 15
Best Local Similarity	100.0%	Pred. No.	1.8e-05	
Matches 15	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	EKPVEAYKAAAP	15
Db	1	EKPVEAYKAAAP	15

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RESULT 2
ABP52291
ID      ABP52291 standard; peptide; 15 AA.
XX

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DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:85

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-B*02; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

OS	Homo sapiens.
OS	Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Frickis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autotumour-specific HLA-DR2-restricted T cell clones. Aβp52307 to Aβp52305 represent peptides used in the exemplification of the present invention.

SQ Sequence 15 AA;

Query Match	93.2%	Score 69	DB 5	Length 15
Best Local Similarity	93.3%	Pred. No. 0.00013		
Matches 14	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY 1 EKPKVEAYKAAAPARA 15
||| ||| ||| |||
Db 1 EKPKYEAYKAAAAPA 15

```

RESULT 3
ABP52297
ID      ABP52297  standard; peptide; 15 AA.

```

DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:91

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-vital encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

OS Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Frickis-Hareli M,

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major PT histocompatibility complex class II HLA-R2 protein, useful for treating a PT demyelinating disease, e.g. multiple sclerosis, or post-viral PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autotantigen-specific, HLA-DR2-restricted T cell clones. ABP52207 to ABP5305 represent peptides used in the exemplification of the present invention

Sequence 15 AA;

Query Match	93.2%	Score 69;	DB 5;	Length 15;
Best Local Similarity	93.3%	Pred. No. 0.00013;		
Matches 14;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 EKPVEAYKAAAPA 15

Db 1 EKPKFEAYKAAAPA 15

RESULT 4

ABP52305 standard; peptide; 15 AA.

XX AC ABP52305;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:99.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; anti-inflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
 OS Synthetic.

PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has anti-inflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention

XX SQ Sequence 15 AA;

Query Match 91.9%; Score 68; DB 5; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.00019;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPA 15
 1 EKPKFEAYKAAAPA 15

RESULT 5
 ABP52300 standard; peptide; 15 AA.

XX ABP52300;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:94.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; anti-inflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
 OS Synthetic.

PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has anti-inflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention

XX SQ Sequence 15 AA;

Query Match 86.5%; Score 64; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.00089;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPA 15
 1 EKPKFEAFKAAAPA 15

RESULT 6
 ABP52290 standard; peptide; 15 AA.

XX ABP52290;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:84.

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; anti-inflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PS New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
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 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agent. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 CC
 SO Sequence 15 AA;
 XX
 SQ
 Query Match 85.1%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKKPEVAYKAAAPA 15
 DB 1 EAPKYEAYKAAAPA 15
 XX
 RESULT 7
 ID ABP52292 standard; peptide; 15 AA.
 XX
 AC ABP52292;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; anti-inflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PS New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
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 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agent. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 CC
 SO Sequence 15 AA;
 XX
 SQ
 Query Match 85.1%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKKPEVAYKAAAPA 15
 DB 1 EAPKYEAYKAAAPA 15
 XX
 RESULT 8
 ID ABP52304 standard; peptide; 15 AA.
 XX
 AC ABP52304;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:98.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; anti-inflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 PD 01-AUG-2002.
 XX

PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
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 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Harell M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 85.1%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKPRVEAYKAAAPA 15
 DB 1 EKPRVEAYKAAAPA 15
 XX
 RESULT 9
 ABP52303
 ID ABP52303 standard; peptide; 17 AA.
 XX
 AC ABP52303;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Harell M;

XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 82.4%; Score 61; DB 5; Length 17;
 Best Local Similarity 86.7%; Pred. No. 0.0033;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKPRVEAYKAAAPA 15
 DB 3 EKPRVEAYKAAAPA 17
 XX
 RESULT 10
 ADN60395
 ID ADN60395 standard; protein; 781 AA.
 XX
 AC ADN60395;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE B. licheniformis sporulation related polypeptide, seq id 67.
 XX
 KM Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;
 KM lyase; isomerase; ligase.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO2003087148-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 25-MAR-2003; 2003WO-DK000200.
 XX
 PR 10-APR-2002; 2002DK-00000533.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen JT, Jorgensen ST, Raasmussen MD, Olsen PB, Clausen IG;
 XX
 DR WPI; 2004-122131/12.
 DR N-PSDB; ADN60394.
 XX
 PT A Bacillus licheniformis mutant host cell for producing a product of
 PT interest e.g. vitamins, antibiotics and enzymes.
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 PS Claim 1; SEQ ID NO 67; 319pp; English.
 XX
 CC The invention relates to a Bacillus licheniformis mutant host cell
 CC derived from a parent B. licheniformis host cell. The mutant host cell is
 CC mutated in one or more genes encoding one or more polypeptides involved

CC in sporulation. The host cell comprises one or more heterologous genes
CC present in at least two copies, encoding one or more heterologous
CC polypeptides. The heterologous genes are stably integrated into the
CC genome of the cell without leaving any antibiotic resistance marker genes
CC at the site of integration. The heterologous genes are transcribed from a
CC heterologous promoter or from an artificial promoter, and are comprised
CC in an operon, preferably a polycistronic operon. The heterologous
CC polypeptide is an antimicrobial peptide, or a fusion peptide comprising a
CC peptide part which in its native form has antimicrobial activity. The
CC heterologous polypeptide is an enzyme, preferably a secreted enzyme. The
CC enzyme is an enzyme of a class selected from the group of enzyme classes
CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC
CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The *Bacillus*
CC licheniformis is useful in a process for producing at least one product
CC of interest, comprising cultivating a *B. licheniformis* mutant host cell
CC in a suitable medium, whereby the said product is produced. The process
CC further comprises isolating or purifying the product of interest. The
CC current sequence represents a *B. licheniformis* sporulation related
CC polypeptide.

CC Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;
Best Local Similarity 73.3%; Pred. No. 0.53;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|:|:|:|
Db 264 EKPEVQAYEAPAPA 278

RESULT 11
ID ADN60505 standard; protein; 781 AA.

XX ADN60505;

DT 01-JUL-2004 (first entry)

DE B. *licheniformis* sporulation related polypeptide, seq id 177.

KM Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;
KW lyase; isomerase; ligase.

XX *Bacillus licheniformis*.

OS WO2003087148-A2.

PN 23-OCT-2003.

PF 25-MAR-2003; 2003WO-DK000200.

PR 10-APR-2002; 2002DK-00000533.

PA (NOVO) NOVOTYMES AS.

PI Andersen JT, Jorgensen ST, Raemussen MD, Olsen PB, Clausen IG;

DR WPI; 2004-122131/12.

PT N-PSDB; ADN60504.

XX A *Bacillus licheniformis* mutant host cell for producing a product of
XX interest e.g. vitamins, antibiotics and enzymes.

XX Claim 1; SEQ ID NO 177; 319pp; English.

CC The invention relates to a *Bacillus licheniformis* mutant host cell
CC derived from a parent *B. licheniformis* host cell. The mutant host cell is
CC mutated in one or more genes encoding one or more polypeptides involved
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CC present in at least two copies, encoding one or more heterologous
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CC genome of the cell without leaving any antibiotic resistance marker genes

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CC peptide part which in its native form has antimicrobial activity. The
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CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC
CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The *Bacillus*
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CC in a suitable medium, whereby the said product is produced. The process
CC further comprises isolating or purifying the product of interest. The
CC current sequence represents a *B. licheniformis* sporulation related
CC polypeptide.

CC Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;
Best Local Similarity 73.3%; Pred. No. 0.53;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|:|:|:|
Db 264 EKPEVQAYEAPAPA 278

RESULT 12
ID ADN60519 standard; protein; 781 AA.

XX ADN60519;

DT 01-JUL-2004 (first entry)

DE B. *licheniformis* sporulation related polypeptide, seq id 191.

KM Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;
KW lyase; isomerase; ligase.

XX *Bacillus licheniformis*.

PN WO2003087148-A2.

PD 23-OCT-2003.

PF 25-MAR-2003; 2003WO-DK000200.

PR 10-APR-2002; 2002DK-00000533.

PA (NOVO) NOVOTYMES AS.

PI Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PB, Clausen IG;

DR WPI; 2004-122131/12.

PT N-PSDB; ADN60518.

XX A *Bacillus licheniformis* mutant host cell for producing a product of
XX interest e.g. vitamins, antibiotics and enzymes.

XX Claim 1; SEQ ID NO 191; 319pp; English.

CC The invention relates to a *Bacillus licheniformis* mutant host cell
CC derived from a parent *B. licheniformis* host cell. The mutant host cell is
CC mutated in one or more genes encoding one or more polypeptides involved
CC in sporulation. The host cell comprises one or more heterologous genes
CC present in at least two copies, encoding one or more heterologous
CC polypeptides. The heterologous genes are stably integrated into the
CC genome of the cell without leaving any antibiotic resistance marker genes
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CC heterologous promoter or from an artificial promoter, and are comprised
CC in an operon, preferably a polycistronic operon. The heterologous
CC polypeptide is an antimicrobial peptide, or a fusion peptide comprising a

CC peptide part which in its native form has antimicrobial activity. The
 CC heterologous polypeptide is an enzyme, preferably a secreted enzyme. The
 CC enzyme is an enzyme of a class selected from the group of enzyme classes
 CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC
 CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The Bacillus
 CC licheniformis is useful in a process for producing at least one product
 CC of interest, comprising culturing a B. licheniformis mutant host cell
 CC in a suitable medium, whereby the said product is produced. The process
 CC further comprises isolating or purifying the product of interest. The
 CC current sequence represents a B. licheniformis sporulation related
 CC polypeptide.

XX
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 SQ Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;
 Best Local Similarity 73.3%; Pred. No. 0.53;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPAA 15
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 DB 264 EKPEVQAYEAPAPAA 278

RESULT 13
 ABP52302
 ID ABP52302 standard; peptide; 17 AA.
 XX
 AC ABP52302;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:96.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.

XX Homo sapiens.
 OS Synthetic.

XX W0200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Harell M;

XX WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52205 represent peptides used in the exemplification of the present
 CC invention

SQ Sequence 17 AA;

Query Match 77.0%; Score 57; DB 5; Length 17;
 Best Local Similarity 80.0%; Pred. No. 0.015;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPAA 15
 |||:|||||
 DB 3 EKAKFEAFKAAAPAA 17

RESULT 14
 ABP52271
 ID ABP52271 standard; peptide; 15 AA.
 XX
 AC ABP52271;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.

XX Homo sapiens.
 OS Synthetic.

XX W0200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

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XX WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
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XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
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 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention

SQ Sequence 15 AA;

Query Match	71.6%;	Score 53;	DB 5;	Length 15;
Best Local Similarity	80.0%;	Pred. No. 0.064;		
Matches 12; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Search completed: February 26, 2005, 23:48:24
Job time : 77.6837 secs

Qy	1	EKPVEAYKAAAP	15
Db	1	EKAKEYEAYKAAAA	15

RESULT 15

ABP52289
ID ABP52289 standard; peptide; 15 AA.

AC ABP52289;

DT 16-OCT-2002 (first entry)

HLA-DR2 molecule binding peptide SEQ ID NO:83.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW immune response; antiinflammatory; neuroprotective; proliferation;

post-viral encephalomyelitis; post-vaccine demyelinating condition;

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05 Synthetic.
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PN MO200259143-A2.
XY

01-AUG-2002
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24-JAN-2002

24-JAN-2001; 200105-0263569P.

PA (HARD) HARVARD COLLEGE
XX

Strominger JL, Flaklis-Hafell M,
XX

DR WFL; 2002-608439/65.
XX

PT New compatibility component

P1 uemyellinating disease

Claim 28: Page 39: 5400: English

The present invention describes compositions (T) comprising a peptide

residues. The complex of the peptide with a major histocompatibility

complex (MHC) class II HLA-DR α protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities.

comprising the peptides are useful for treating demyelinating diseases and can be used as a MHC class II protein inhibitor. The compositions

demethylating condition, and a side effect of administering an anti-

of autoantigen-specific HLA-DR2-restricted T cell clones, ABP52207 to

CC represents papers used in the exemplification of the present
CC invention

Sequence 15 AA:

Query Match 71.6%; Score 53; DB 5; Length 15;

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2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2536-2537-2538-2539-2540-2541-2542-2543-2544-2545-2546-2547-2548-2549-2550-2551-2552-2553-2554-2555-2556-2557-2558-2559-2560-2561-2562-2563-2564-2565-2566-2567-2568-2569-2570-2571-2572-2573-2574-2575-2576-2577-2578-2579-2580-2581-2582-2583-2584-2585-2586-2587-2588-2589-2590-2591-2592-2593-2594-2595-2596-2597-2598-2599-2600-2601-2602-2603-2604-2605-2606-2607-2608-2609-2610-2611-2612-2613-2614-2615-2616-2617-2618-2619-2620-2621-2622-2623-2624-2625-2626-2627-2628-2629-2630-2631-2632-2633-2634-2635-2636-2637-2638-2639-2640-2641-2642-2643-2644-2645-2646-2647-2648-2649-2650-2651-2652-2653-2654-2655-2656-2657-2658-2659-2660-2661-2662-2663-2664-2665-2666-2667-2668-2669-2670-2671-2672-2673-2674-2675-2676-2677-2678-2679-2680-2681-2682-2683-2684-2685-2686-2687-2688-2689-2690-2691-2692-2693-2694-2695-2696-2697-2698-2699-2700-2701-2702-2703-2704-2705-2706-2707-2708-2709-2710-2711-2712-2713-2714-2715-2716-2717-2718-2719-2720-2721-2722-2723-2724-2725-2726-2727-2728-2729-2730-2731-2732-2733-2734-2735-2736-2737-2738-2739-2740-2741-2742-2743-2744-2745-2746-2747-2748-2749-2750-2751-2752-2753-2754-2755-2756-2757-2758-2759-2760-2761-2762-2763-2764-2765-2766-2767-2768-2769-2770-2771-2772-2773-2774-2775-2776-2777-2778-2779-2780-2781-2782-2783-2784-2785-2786-2787-2788-2789-2790-2791-2792-2793-2794-2795-2796-2797-2798-2799-2800-2801-2802-2803-2804-2805-2806-2807-2808-2809-2810-2811-2812-2813-2814-2815-2816-2817-2818-2819-2820-2821-2822-2823-282
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1 EKPVEAYKAAAPA 15

Db 1 EAPAYKAYKAAAPAA 15

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Title: US-10-056-583A-93
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Sequence: 1 EKPVEAYKAAAPA 15

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 513545

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	42	56.8	1402	3	US-09-004-838-11
3	41	55.4	297	4	US-09-252-991A-18932
4	40	54.1	75	4	US-09-513-999C-5101
5	40	54.1	222	4	US-09-949-016-9547
6	40	54.1	501	4	US-09-902-540-11248
7	39	52.7	76	4	US-09-270-767-61694
8	39	52.7	197	4	US-09-902-540-12825
9	39	52.7	435	4	US-09-949-016-7245
10	38.5	52.0	170	6	5215917-2
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14	38	51.4	122	4	US-09-270-767-15661
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16	38	51.4	159	4	US-09-732-210-832
17	38	51.4	208	4	US-09-902-540-16427
18	38	51.4	488	4	US-08-928-692-10
19	38	51.4	605	4	US-09-339-972-10
20	38	51.4	688	4	US-08-714-741-46
21	38	51.4	642	4	US-09-489-039A-12434
22	38	51.4	1192	4	US-09-902-540-12662
23	37	50.0	72	4	US-09-621-976-3951
24	37	50.0	80	4	US-09-902-540-14758
25	37	50.0	132	3	US-09-724-864-65
26	37	50.0	142	4	US-09-949-016-10395
27	37	50.0	155	4	US-09-732-210-836

28	37	50.0	211	4	US-09-276-438-5	Sequence 5, Appli
29	37	50.0	251	4	US-09-902-540-14930	Sequence 14930, A
30	37	50.0	341	4	US-09-902-540-14167	Sequence 14167, A
31	37	50.0	861	4	US-09-949-016-10418	Sequence 10418, A
32	37	50.0	1387	4	US-09-902-540-11948	Sequence 11948, A
33	37	50.0	1431	4	US-09-902-540-10614	Sequence 10614, A
34	36.5	49.3	168	4	US-09-479-040-7	Sequence 7, Appli
35	36	48.6	60	1	US-08-346-849-16	Sequence 16, Appli
36	36	48.6	60	2	US-08-293-284A-16	Sequence 16, Appli
37	36	48.6	60	4	US-08-898-300-16	Sequence 16, Appli
38	36	48.6	60	4	US-08-824-513-16	Sequence 16, Appli
39	36	48.6	61	4	US-09-270-767-62451	Sequence 62451, A
40	36	48.6	125	4	US-09-770-834-11	Sequence 11, Appli
41	36	48.6	141	4	US-09-902-540-10465	Sequence 10465, A
42	36	48.6	193	4	US-09-252-991A-21712	Sequence 21712, A
43	36	48.6	290	4	US-09-358-1383C-8	Sequence 8, Appli
44	36	48.6	340	4	US-09-543-681A-7850	Sequence 7850, Ap
45	36	48.6	351	4	US-09-809-665A-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-004-838-14
Sequence 14, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Binhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-07881005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY:
LOCATION: 1..314
OTHER INFORMATION: /note= "RLGID amino acids"
US-09-004-838-14

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Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKEAYKAA 11
DB 114 EKPKEAYKAA 124

RESULT 2
US-09-004-838-11
Sequence 11, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elmhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: -
LOCATION: 1..1402
OTHER INFORMATION: /note= "RUGIA amino acids"
US-09-004-838-11

Query Match 56.8%; Score 42; DB 3; Length 1402;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKEAYKAA 11
DB 515 EKPKEAYKAA 525

RESULT 3
US-09-252-991A-18932
Sequence 18932, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18932
LENGTH: 297
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18932

Query Match 55.4%; Score 41; DB 4; Length 297;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 EKPKEAYKAAAPA 15
DB 214 DRPAADRYNAAAPA 228

RESULT 4
US-09-513-999C-5101
Sequence 5101, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5101
LENGTH: 75
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-5101

Query Match 54.1%; Score 40; DB 4; Length 75;
Best Local Similarity 64.3%; Pred. No. 9.3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 KPEKEAYKAAAPA 15
DB 7 EKPKEAYKAPAPA 20

RESULT 5
US-09-949-016-9547
Sequence 9547, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03


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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9547
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9547
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Best Local Similarity 64.3%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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OY      2 KPKVEAYKAAAP 15
Db      32 EPKKAAKPAAP 45
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RESULT 6

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US-09-902-540-11248
; Sequence 11248; Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ. ID NOS: 16825
; SEQ ID NO 11248
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11248
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Best Local Similarity 57.1%; Pred. No. 74;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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OY      1 EKPVEAYKAAAP 14
Db      258 EKPVADLRVAAP 271
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RESULT 7

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US-09-270-767-61694
; Sequence 61694; Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ. ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 61694
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61694
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Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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OY      2 KPKVEAYKAAAP 14
Db      14 KPKTKYKAKQTP 26
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RESULT 8

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US-09-902-540-12825
; Sequence 12825; Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ. ID NOS: 16825
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; ORGANISM: Myxococcus xanthus
US-09-902-540-12825
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OY      1 EKPVEAYKAAAP 15
Db      19 EEPAAEKPAAP 33
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RESULT 9

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; Sequence 7245; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7245
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Best Local Similarity 46.7%; Pred. No. 94;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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Db      336 QPPALAKYPAAP 350
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RESULT 10

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; Patent No. 5215917
; APPLICANT: DE ARAUJO, FAUSTO G.; PRINCE, JEFFREY B.; REMINGTON,
; JACK S.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING THE TOXOPLASMA
; GONDI P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
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5215917-2

Query Match          52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
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Db 99 EKPOVLCKVCVAEAGAPA 116

RESULT 11
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; Patent No. 5472844
; APPLICANT: DE ARAUJO, FAUSTO G.; PRINCE, JEFFREY B.;
; REMINGTON JACK S.
; TITLE OF INVENTION: METHODS OF DETECTION OF TOXOPLASMA
; GONDI P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,540
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 24,932
; FILING DATE: 02-MAR-1993
; APPLICATION NUMBER: 431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5472844-2

Query Match          52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 EKPKVEAYKA--AAAPA 15
   |||:| |||
Db 99 EKPOVLCKVCVAEAGAPA 116

RESULT 12
5215917-2
; Patent No. 5215917
; APPLICANT: DE ARAUJO, FAUSTO G.; PRINCE, JEFFREY B.; REMINGTON,
; JACK S.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING THE TOXOPLASMA
; GONDI P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5215917-2

Query Match          52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 EKPKVEAYKA--AAAPA 15
   |||:| |||
Db 99 EKPOVLCKVCVAEAGAPA 116
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RESULT 13
5472844-2
; Patent No. 5472844
; APPLICANT: DE ARAUJO, FAUSTO G.; PRINCE, JEFFREY B.;
; REMINGTON JACK S.
; TITLE OF INVENTION: METHODS OF DETECTION OF TOXOPLASMA
; GONDI P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,540
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 24,932
; FILING DATE: 02-MAR-1993
; APPLICATION NUMBER: 431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5472844-2

Query Match          52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 EKPKVEAYKA--AAAPA 15
   |||:| |||
Db 99 EKPOVLCKVCVAEAGAPA 116

RESULT 14
US-09-270-767-35661
; Sequence 35661, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35661
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35661

Query Match          51.4%; Score 38; DB 4; Length 122;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAA 11
   ||||| |||
Db 34 EKPKVEVLSAA 44

RESULT 15
US-09-270-767-50878
; Sequence 50878, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50878
```

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:      LENGTH: 122
:
:      TYPE: prt
:
:      ORGANISM: Drosophila melanogaster
:
:      FEATURE:
:
:      OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50878

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Query Match	51.4%	Score 38	DB 4	Length 122
Best Local Similarity	72.7%	Pred. No. 35		
Matches	8	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0

Qy 1 EKRPVEAYKAA 11
|||
||
Db 34 EKRPVEVLSAA 44

Search completed: February 26, 2005, 23:59:30
Job time : 21.051 secs

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GenCore version 5.1.6
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OM protein - prdtein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 53.5714 Seconds

(Without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583A-93

Perfect score: 74

Sequence: 1 EKPKVEAYKAAAPA 15

Scoring table: BIOSCM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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19: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pep:*

20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	US-10-056-583-93	Sequence 93, Appl
2	69	93.2	15	US-10-056-583-85	Sequence 85, Appl
3	69	93.2	15	US-10-056-583-91	Sequence 91, Appl
4	68	91.9	15	US-10-056-583-99	Sequence 99, Appl
5	64	86.5	15	US-10-056-583-94	Sequence 94, Appl
6	63	85.1	15	US-10-056-583-84	Sequence 84, Appl
7	63	85.1	15	US-10-056-583-86	Sequence 86, Appl
8	63	85.1	15	US-10-056-583-98	Sequence 98, Appl
9	61	82.4	17	US-10-056-583-97	Sequence 97, Appl
10	57	77.0	17	US-10-056-583-96	Sequence 96, Appl
11	53	71.6	15	US-10-056-583-65	Sequence 65, Appl
12	53	71.6	15	US-10-056-583-83	Sequence 83, Appl
13	53	71.6	17	US-10-056-583-88	Sequence 88, Appl

14	53	71.6	17	US-10-056-583-90	Sequence 90, Appl
15	53	71.6	19	US-10-056-583-89	Sequence 89, Appl
16	52	70.3	15	US-10-056-583-92	Sequence 92, Appl
17	49	66.2	15	US-10-056-583-87	Sequence 87, Appl
18	49	66.2	15	US-10-056-583-95	Sequence 95, Appl
19	47	63.5	15	US-10-056-583-64	Sequence 64, Appl
20	47	63.5	15	US-10-056-583-66	Sequence 66, Appl
21	45	60.8	14	US-10-056-583-57	Sequence 57, Appl
22	43	58.1	15	US-10-056-583-51	Sequence 51, Appl
23	43	58.1	15	US-10-056-583-53	Sequence 53, Appl
24	43	58.1	15	US-10-056-583-58	Sequence 58, Appl
25	43	58.1	15	US-10-056-583-61	Sequence 61, Appl
26	43	58.1	15	US-10-056-583-63	Sequence 63, Appl
27	42	56.8	15	US-10-056-583-65	Sequence 65, Appl
28	41	55.4	15	US-10-056-583-67	Sequence 67, Appl
29	41	55.4	15	US-10-056-583-69	Sequence 69, Appl
30	41	55.4	15	US-10-056-583-71	Sequence 71, Appl
31	41	55.4	15	US-10-056-583-73	Sequence 73, Appl
32	41	55.4	15	US-10-056-583-75	Sequence 75, Appl
33	41	55.4	15	US-10-056-583-77	Sequence 77, Appl
34	41	55.4	15	US-10-056-583-79	Sequence 79, Appl
35	40	54.1	15	US-10-056-583-81	Sequence 81, Appl
36	40	54.1	15	US-10-056-583-83	Sequence 83, Appl
37	40	54.1	15	US-10-056-583-85	Sequence 85, Appl
38	40	54.1	15	US-10-056-583-87	Sequence 87, Appl
39	40	54.1	15	US-10-056-583-89	Sequence 89, Appl
40	40	54.1	15	US-10-056-583-91	Sequence 91, Appl
41	40	54.1	15	US-10-056-583-93	Sequence 93, Appl
42	40	54.1	15	US-10-056-583-95	Sequence 95, Appl
43	40	54.1	15	US-10-056-583-97	Sequence 97, Appl
44	40	54.1	15	US-10-056-583-99	Sequence 99, Appl
45	40	54.1	15	US-10-056-583-01	Sequence 01, Appl

ALIGNMENTS

RESULT 1

US-10-056-583-93

Sequence 93, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: President and Fellows of Harvard College

APPLICANT: Fiddis-Harell, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DENEUTRINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 93

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-93

Query Match

Best Local Similarity 100.0%; Score 74; DB 14; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15

DB 1 EKPKVEAYKAAAPA 15

RESULT 2

US-10-056-583-85

```
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
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Query Match          93.2%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 5,7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKVEAYKAAAPA 15
Db      1 EKPKVEAYKAAAPA 15
```

```
RESULT 3
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
```

```
Query Match          93.2%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 5,7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKVEAYKAAAPA 15
Db      1 EKPKVEAYKAAAPA 15
```

```
RESULT 4
US-10-056-583-99
; Sequence 99, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
```

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Query Match          91.9%; Score 68; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 8,5e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKVEAYKAAAPA 15
Db      1 EKPKVEAYKAAAPA 15
```

```
RESULT 5
US-10-056-583-94
; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94
```

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Query Match          86.5%; Score 64; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0,00041;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKVEAYKAAAPA 15
Db      1 EKPKVEAYKAAAPA 15
```

```
RESULT 6
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```

RESULT 10.
US-10-056--583-96
? Sequence 96, Application US/10055583
? Publication No. US20030064915A1
? GENERAL INFORMATION:
? APPLICANT: President and Fellows of Harvard College
? APPLICANT: Strominger, Jack L.
? APPLICANT: Fridlis-Hareli, Masna
? TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
? TITLE OF INVENTION: CONDITIONS
? FILE REFERENCE: 24655-017
? CURRENT APPLICATION NUMBER: US/10/056,583
? CURRENT FILING DATE: 2002-01-24
? PRIOR APPLICATION NUMBER: 60/263,569
? PRIOR FILING DATE: 2001-01-24
? NUMBER OF SEQ ID NOS: 99
? SOFTWARE: FaetSeq for Windows Version 4.0
? SEQ ID NO 96
? LENGTH: 17
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:

```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match 77.0%; Score 57; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0073;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|||||
DB 3 EKAKFEAFKAAAPA 17

RESULT 11

US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match 71.6%; Score 53; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|||||
DB 1 EKAKVEAYKAAAPA 15

RESULT 12
US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-83

Query Match 71.6%; Score 53; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.031;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|||||
DB 1 EAPAYKAAAPA 15

RESULT 13
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match 71.6%; Score 53; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.035;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|||||
DB 3 EKAKVEAYKAAAPA 17

RESULT 14
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match 71.6%; Score 53; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.035;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15
|||:|||||
DB 1 EKAKVEAYKAAAPA 15

RESULT 15

US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

Query Match 71.6%; Score 53; DB 14; Length 19;
Best Local Similarity 80.0%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EKPKVEAYKAAAP 15
Db 3 EKAKVEAYKAAAP 17

Search completed: February 27, 2005, 00:05:23
Job time : 53.5714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 13.3163 Seconds
(without alignment)
108.382 Million cell updates/sec

Title: US-10-056-583a-93

Perfect score: 74

Sequence: 1 EKPKEVAYKAAAPAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	64.9	389	2 G87332	hypothetical prote
2	45	60.8	193	1 MOWS4E	myosin alkali ligh
3	45	60.8	306	2 G96014	hypothetical prote
4	45	60.8	765	2 T15447	hypothetical prote
5	43	58.1	50	2 G97151	hypothetical prote
6	43	58.1	270	2 T31225	traf protein hemol
7	43	58.1	428	2 E87463	hypothetical prote
8	42	56.8	185	1 MOWS4E	myosin alkali ligh
9	42	56.8	193	1 MOWS4E	myosin alkali ligh
10	42	56.8	200	2 T48130	hypothetical prote
11	42	56.8	337	2 C70473	phosphate-binding
12	42	56.8	398	2 T21061	hypothetical prote
13	42	56.8	461	2 A13358	pyruvate dehydroge
14	42	56.8	656	2 AE1479	probable cell surf
15	41	55.4	168	2 A45943	vitelline membrane
16	41	55.4	336	1 S75272	cytochrome d ubiqu
17	41	55.4	810	2 C95401	probable oxidoredu
18	40	54.1	114	2 G81353	hypothetical prote
19	40	54.1	197	1 MOWS4E	myosin alkali ligh
20	40	54.1	300	2 H87631	integral membrane
21	40	54.1	452	2 T25076	hypothetical prote
22	40	54.1	586	2 T29657	hypothetical prote
23	40	54.1	729	2 T51896	probable translati
24	40	54.1	891	2 AC3384	ribonuclease B / z
25	39	52.7	145	2 T13350	hypothetical prote
26	39	52.7	179	2 F97683	50S ribosomal prot
27	39	52.7	179	2 AF2908	50S ribosomal prot
28	39	52.7	231	2 S18006	histone H1 - midge
29	39	52.7	379	2 T08277	carotenoid biosynt

30	39	52.7	508	2 S19266	anthranilate synth
31	39	52.7	594	1 D55514	dihydroliposamide d
32	39	52.7	688	1 H96681	protein F1E2.10 l
33	39	52.7	723	2 AG3555	histidine ammonia-
34	38.5	52.0	166	2 A44968	surface antigen P2
35	38.5	52.0	447	2 AB3359	dihydroliposamide S
36	38.5	52.0	762	2 H87302	chemotaxis protein
37	38	51.4	98	2 T20034	photosystem I chai
38	38	51.4	160	2 TC2012	ribosomal protein
39	38	51.4	225	2 T05334	endomembrane-assoc
40	38	51.4	246	2 H71548	hypothetical prote
41	38	51.4	346	2 AH2308	cytochrome D ubiqu
42	38	51.4	353	2 AB1823	hypothetical prote
43	38	51.4	546	2 T06415	calnexin - soybean
44	38	51.4	622	2 T29508	hypothetical prote
45	38	51.4	629	2 AH0521	dihydroliposamide a

ALIGNMENTS

RESULT 1

G87332 hypothetical protein CC0674 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87332

R:Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87332

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <STO>

A:Cross-references: UNIPROT:Q9NAC8; GB:AE05673; NID:G13421893; PIDN:AAK22659.1; GSPDB:

C:Genetic8;

A:Gene: CC0674

Query Match 64.9%; Score 48; DB 2; Length 389;
Best Local Similarity 71.4%; Pred. No. 2.3;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKVEAYKAAAPAA 15

Db 66 KTSVETFKAAAPAA 79

RESULT 2

MOWS4E myosin alkali light chain 4, embryonic and atrial - mouse

N:Alternate names: MLC1A; MLC1emb; myosin I1 catalytic light chain, atrial

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: A31114; S01944

J. Biol. Chem. 263, 12659-12676, 1988

A:Title: Structure and sequence of the myosin alkali light chain gene expressed in adult

A:Reference number: A31114; MUID:88315068; PMID:2842339

A:Accession: A31114

A:Molecule type: DNA

A:Residues: 1-193 <BAR>

A:Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:G199731; PIDN:

R:Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.

Nucleic Acids Res. 16, 10037-10052, 1988

A:Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striat

A:Reference number: S01944; MUID:89057447; PMID:3194193

A:Accession: S01944

A:Molecule type: DNA

A:Residues: 1-41 <COH>

A:Cross-references: EMBL:X12971; NID:G53138; PIDN:CAA31414.1; PID:G53139

C/Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fetal
C/Genetics:
A:Introns: 41/3; 51/1; 101/1; 159/1; 185/1
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract
F:47-81/Domain: calmodulin repeat homology <EF1>
F:156-158/Domain: calmodulin repeat homology <EF3>
F:161-193/Domain: calmodulin repeat homology <EF4>

Query Match 60.8%; Score 45; DB 1; Length 193;
Best Local Similarity 71.4%; Pred. No. 3.7;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPRVEAYKAAAPA 15
DB 7 EPKEAAKPAAPA 20

RESULT 3
G96014
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymH
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: G96014
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernat
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:11461431
A/Accession: G96014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-306 <KUR>
A/Cross-references: UNIPROT:Q92TW2; GB:AL591985; PIDN:CAC49783.1; PID:g15141270; GSPDB:C
A/Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punter, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pel, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
C/Contents: annotation
C/Genetics:
A/Gene: Smb20676
A/Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 306;
Best Local Similarity 57.1%; Pred. No. 5.8;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPRVEAYKAAAPA 15
DB 66 RPOPEAFESAAAPA 79

RESULT 4
T15447
hypothetical protein C07G1.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15447
R:Hawkins, J.
submitted to the EMBL Data Library, May 1996
A/Description: The sequence of C. elegans cosmid C07G1.
A/Reference number: Z18352
A/Accession: T15447
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-765 <HAW>
A/Cross-references: UNIPROT:Q17796; EMBL:U58751; NID:g1326379; PID:g1326382; PIDN:AAB006
A/Experimental source: strain Bristol N2; clone C07G1
C/Genetics:

A/Gene: CESP:C07G1.5
A/Map position: 4
A:Introns: 33/3; 46/1; 74/2; 136/3; 554/3; 681/1; 742/1

Query Match 60.8%; Score 45; DB 2; Length 765;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPRVEAYKAAAP 14
DB 326 KPEVDGYKAAAB 338

RESULT 5
G97151
hypothetical protein CAC2043 [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: G97151
R:Nolling, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G97151
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-50 <KUR>
A/Cross-references: UNIPROT:Q97HG8; GB:AE001437; PIDN:AAK80002.1; PID:g15025028; GSPDB:C
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC2043

Query Match 58.1%; Score 43; DB 2; Length 50;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPRVAYK 9
DB 35 EKPRVAYK 43

RESULT 6
T31225
traf protein homolog - Sphingomonas aromaticivorans plasmid pNL1
C/Species: Sphingomonas aromaticivorans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T31225
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.;
submitted to the EMBL Data Library, July 1998
A/Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
A/Reference number: Z20992
A/Accession: T31225
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-270 <ROM>
A/Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:g3378261; PID:g3378366; PIDN:AAD0
A/Genetics:
A/Genome: plasmid pNL1
A/Note: traf

Query Match 58.1%; Score 43; DB 2; Length 270;
Best Local Similarity 76.9%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPRVAYKAAAP 13
DB 54 EKPRVAYKAAAP 66

RESULT 7
E87463
hypothetical protein CC1729 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: E87463
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Leub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolor, N.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: E87463
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-428 <STO>
 A/Cross-references: UNIPROT:Q9A7J4; GB:AE005673; NID:G13423147; PID:AAK23705.1; GSPDB:C
 C/Genetics:
 A/Gene: CCI729
 C/Superfamily: dhydrolipamide acetyltransferase, lipoyl/biotin-binding homology

Query Match 58.1%; Score 43; DB 2; Length 428;
 Best Local Similarity 90.9%; Pred. No. 17;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 PKVEAYKAAAP 13
 |||||
 Db 88 PKVEAPKAAAP 98

RESULT 8

MOCH4E

myosin alkali light chain 4, embryonic - chicken
 N/Alternate names: myosin I23 catalytic light chain
 C/Species: Gallus gallus (chicken)
 C/Date: 01-Dec-1999 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S02065; A29473
 R/Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriyama, J. Mol. Biol. 204, 497-505, 1998
 A/Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic g
 A/Reference number: S02065; MUID:69141751; PMID:3225843
 A/Accession: S02065
 A/Molecule type: DNA
 A/Residues: 1-185 <NAB>
 A/Cross-references: UNIPROT:P09540; EMBL:X14428
 A/Note: the authors translated the codon CCG for residue 71 as Ala
 R/Kawashima, M.; Nabeshima, Y.; Oshinata, T.; Fujii-Kuriyama, Y.
 J. Biol. Chem. 262, 14408-14414, 1987
 A/Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac
 A/Reference number: A29473; MUID:88032983; PMID:3667580
 A/Accession: A29473
 A/Molecule type: mRNA
 A/Residues: 1-93, 'L', 95-165, 'L', 167-185 <KAW>
 A/Cross-references: GB:J02823; NID:G212339; PID:AAA48957.1; PID:G212340
 A/Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1
 C/Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac
 C/Genetics:
 A/Intons: 33/3; 43/1; 93/1; 151/1; 177/1
 C/Superfamily: The myosin molecule contains two heavy chains, two alkali light chains, and t
 C/Keywords: brain; calcium binding; duplication; EF hand; muscle contraction
 F/39-73/Domain: calmodulin repeat homology <EF1>
 F/118-150/Domain: calmodulin repeat homology <EF3>
 F/153-185/Domain: calmodulin repeat homology <EF4>

Query Match 56.8%; Score 42; DB 1; Length 185;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PKVEAYKAAAP 14
 |||||
 Db 8 PKVDAAKAAAP 19

RESULT 9

MORT4E

myosin alkali light chain 4, embryonic and atrial - rat
 N/Alternate names: MCL1A; MCL1emb; myosin I1 catalytic light chain, atrial
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 29-Jan-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S09236
 R/Rovner, A.S.; McNally, E.M.; Leinwand, L.A.
 Nucleic Acids Res. 18, 1581-1596, 1990
 A/Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of express
 A/Reference number: S09236; MUID:50221887; PMID:2236197
 A/Accession: S09236
 A/Molecule type: mRNA
 A/Residues: 1-193 <ROV>
 A/Cross-references: UNIPROT:P17209; EMBL:X51531; NID:957512; PID:CAA35911.1; PID:95751
 C/Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fe
 C/Superfamily: calmodulin; calmodulin repeat homology
 C/Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contra
 F/47-81/Domain: calmodulin repeat homology <EF1>
 F/126-158/Domain: calmodulin repeat homology <EF3>
 F/161-193/Domain: calmodulin repeat homology <EF4>

Query Match 56.8%; Score 42; DB 1; Length 193;
 Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 KPKVEAYKAAAP 15
 |||||
 Db 7 EPKKEAKVAAAP 20

RESULT 10

T48130

hypothetical protein T4C9.40 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C/Accession: T48130
 R/Beyan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Me
 submitted to the Protein Sequence Database, June 1999
 A/Reference number: Z24485
 A/Accession: T48130
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-200 <BEV>
 A/Cross-references: UNIPROT:Q9STJ1; EMBL:AL080318
 A/Experimental source: cultivar Columbia; BAC clone T4C9
 C/Genetics:
 A/Map position: 4
 A/Intons: 132/1
 A/Note: T4C9.40

Query Match 56.8%; Score 42; DB 2; Length 200;
 Best Local Similarity 69.2%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKPKVEAYKAAAP 13
 |||||
 Db 180 EKPKVEAYKAAAP 192

RESULT 11

C70473

phosphate-binding periplasmic protein - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: C70473
 R/Dickert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
 V.
 Nature 392, 353-358, 1998
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A/Reference number: A70500; MUID:38196666; PMID:9537320
 A/Accession: C70473
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-337 <AQF>

A:Cross-references: UNIPROT:Q67815; GB:AE000768; NID:G2984249; PIDN:AAC07783.1; PID:G298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: psts
C:Superfamily: phosphate-repressible phosphate-binding protein

Query Match 56.8%; Score 42; DB 1; Length 337;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPEVYKAAAPA 15
| : : : : : |
Db 239 KPEITFQAAANA 252

RESULT 12

T21061
Hypothetical protein F17C11.9 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21061

R:McMurray, A.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19366

A:Accession: T21061

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-398 <WIL>

A:Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDN:CAA96631.1; GSPDB:GN00023; CESP:F1

A:Experimental source: clone F17C11

C:Genetics:

A:Gene: CESP:F17C11.9

A:Map position: 5

A:Introns: 3/3; 44/3; 151/3; 196/1; 354/3

C:Superfamily: translation elongation factor eEF-1 gamma chain

Query Match 56.8%; Score 42; DB 2; Length 398;
Best Local Similarity 76.9%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPVEAYKAAAPA 13
| : : : : : |
Db 214 EKPKEAKKAAAPA 226

RESULT 13

A13358

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) [imported] - *Brucella melitensis* (strain

C:Species: *Brucella melitensis*

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 12-Jul-2004
C:Accession: A13358

R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Iov, T.; Ivanova,

proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A>Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A:Reference number: AD2552; PMID:11756688

A:Accession: A13358

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-461 <KUR>

A:Cross-references: UNIPROT:Q9YH6; GB:AE008917; PIDN:AAL52036.1; PID:G17982802; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10855

A:Map position: 1

C:Superfamily: pyruvate dehydrogenase complex, E1 component, beta subunit

C:Keywords: oxidoreductase

Query Match 56.8%; Score 42; DB 2; Length 461;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKPVEAYKAAAPA 15

Db 100 EEPKAEENKADAVPA 114
| : : : : : |

RESULT 14

AE1479

probable cell surface protein (LPXTG motif) [imported] - *Listeria innocua* (strain C11p1)

C:Species: *Listeria innocua*

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1479

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunert, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schluter, T.; Simoes, N.; Tlerriz, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,

A>Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AE1479

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-656 <GLA>

A:Cross-references: UNIPROT:Q92ET6; GB:AL592022; PIDN:CAC95605.1; PID:G16412801; GSPDB:G

A:Experimental source: strain C11p1262

C:Genetics:

A:Gene: lln0372

Query Match 56.8%; Score 42; DB 2; Length 656;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KYEAYKAAAPA 15
| : : : : : |
Db 26 KIDAYKAAAPA 37

RESULT 15

A45943

vitellogenin membrane protein 26A-4 precursor - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A45943

R:Popodi, E.; Minoo, P.; Burke, T.; Waring, G.L.

Dev. Biol. 127, 248-256, 1988

A>Title: Organization and expression of a second chromosome follicle cell gene cluster

A:Reference number: A45943; MUID:88242923; PMID:3132408

A:Accession: A45943

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <POP>

A:Cross-references: UNIPROT:P13238; GB:M20936; NID:G158728; PID:G158729

A:Gene: FlyBase:Vmd6AB

A:Cross-references: FlyBase:FBgn0003980

Query Match 55.4%; Score 41; DB 2; Length 168;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVEAYKAAAPA 15
| : : : : : |
Db 67 PAAQVSAAPADA 79

Search completed: February 26, 2005, 23:57:17
Job time: 14.3163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 65,2041 Seconds

(without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583A-93

Sequence: 1 EKPKEVAYKAAAPA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	78.4	781	2 065JG3	065JG3 bacillus li
2	48	64.9	299	1 RL22 DROME	P50887 drosophila
3	48	64.9	312	2 09UAT1	Q9UAN1 drosophila
4	48	64.9	389	2 09AAC8	Q9AAC8 caulobacter
5	47	63.5	458	2 07SDS7	Q7SDS7 neurospora
6	46	62.2	555	2 07NVT5	Q7NVT5 chromobacte
7	46	62.2	1923	2 07S9W8	Q7S9W8 neurospora
8	45	60.8	192	1 MLEF MOUSE	P09541 mus musculu
9	45	60.8	299	2 06YST4	Q6YST4 oryza sativ
10	45	60.8	306	2 092TW2	Q92TW2 rhizobium m
11	45	60.8	439	2 0869Y7	Q869Y7 dictyosteli
12	45	60.8	729	2 017796	Q17796 caenorhabdi
13	44	59.5	238	1 SSB SHEON	Q8E81 sheenella
14	44	59.5	342	2 062IT6	Q62IT6 burkholderi
15	44	59.5	342	2 063V82	Q63V82 burkholderi
16	44	59.5	447	2 08X0Q2	Q8X0Q2 neurospora
17	44	59.5	462	2 092RQ1	Q92RQ1 arabidopsis
18	44	59.5	464	2 09FLQ4	Q9FLQ4 arabidopsis
19	44	59.5	574	2 08SKW8	Q8SKW8 drosophila
20	44	59.5	607	2 09W327	Q9W327 drosophila
21	43	58.1	50	2 097H88	Q97H88 clostridium
22	43	58.1	136	2 08FR15	Q8FR15 corynebacte
23	43	58.1	143	2 08KG95	Q8KG95 chlorobium
24	43	58.1	227	2 095XQ6	Q95XQ6 caenorhabdi
25	43	58.1	270	2 0859J3	Q859J3 sphingomonas
26	43	58.1	280	2 08U3Y4	Q8U3Y4 pyrococcus
27	43	58.1	428	2 09A7J4	Q9A7J4 caulobacter
28	43	58.1	613	2 08RY21	Q8RY21 oryza sativ
29	42.5	57.4	214	2 0881D7	Q881D7 pseudomonas
30	42	56.8	121	2 089NE4	Q89NE4 bradyrhizob
31	42	56.8	163	2 06JRS4	Q6JRS4 equus cabal

32	42	56.8	185	1 MLEF CHICK	P09540 gallus gall
33	42	56.8	192	1 MLEF RAT	P17209 rattus norv
34	42	56.8	200	2 09STI1	Q9STI1 arabidopsis
35	42	56.8	249	2 0892F2	Q892F2 clostridium
36	42	56.8	283	2 06A7J7	Q6A7J7 propionibac
37	42	56.8	337	2 0678J5	Q678J5 aquifex ae
38	42	56.8	359	2 06C8W3	Q6C8W3 yarrowia li
39	42	56.8	365	2 08BG01	Q8BG01 m mus muscu
40	42	56.8	373	2 0814K9	Q814K9 caenorhabdi
41	42	56.8	398	1 EF1G CAEBL	P54412 caenorhabdi
42	42	56.8	437	1 FLHF PSEPU	O52256 pseudomonas
43	42	56.8	461	2 08YHE6	Q8YHE6 bruceella me
44	42	56.8	461	2 08GOC7	Q8GOC7 bruceella su
45	42	56.8	629	2 09DEI6	Q9DEI6 oreochromis

ALIGNMENTS

RESULT 1					
ID	065JG3	PRELIMINARY;	PRT;	781 AA.	
AC	065JG3;				
DT	25-OCT-2004 (TREMBlrel. 28, Created)				
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)				
DE	SpotITE (DNA translocase)				
GN	Name=spotITE; ORFName=BL01204, BL010906;				
OS	Bacillus licheniformis DSM 13.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=279010;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=DSM 13;				
RX	PubMed=15383718;				
RA	Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,				
RA	Bhrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,				
RA	Ehrenreich A., Gottschalk G.,				
RT	"The Complete Genome Sequence of Bacillus licheniformis DSM13, an				
RT	Organism with Great Industrial Potential."				
RL	J. Mol. Microbiol. Biotechnol. 7:204-211(2004).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 14580;				
RA	Key M.W., Ramatya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,				
RA	Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,				
RA	Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,				
RA	Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,				
RA	Berka R.M.,				
RT	"Complete genome sequence of the industrial bacterium Bacillus				
RT	licheniformis and comparisons with closely related Bacillus species."				
RL	Genome Biol. 5:R77-R77(2004).				
DR	EMBL; AB017333; AAU40801.1; -				
DR	EMBL; CP000002; AAU23441.1; -				
SQ	SEQUENCE 781 AA; 86477 MW; 63495AC2DA5D3D8 CRC64;				
Query Match 78.4%; Score 58; DB 2; Length 781;					
Best Local Similarity 73.3%; Pred. No. 0.51;					
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 EKPKEVAYKAAAPA 15				
Db	264 EKPKEVAYKAAAPA 278				
RESULT 2					
ID	RL22 DROME	STANDARD;	PRT;	299 AA.	
AC	P50887; Q9V3X9;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	25-JAN-2005 (Rel. 46, Last annotation update)				
DE	60S ribosomal protein l22.				

GN Name=RpL22; ORFNames=CG7434;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RA Glover C.V.C., Bidwai A.P., Zhao W.F.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731137; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anagnostis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
 RA Burrows K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keichum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry B., Murphy L., Muszy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mitra S., Crosby W.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Betencourt B.R., Celiker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
 RA Benos P.V., Galt M.C., Ashburner M., Murphy L., Harris D.,
 RA Barelli B.G., Ferraz C., Vidal S., Brun C., Demalbert J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Gallibert F., Borokova D.,
 RA Minana B., Katatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

RA Papagiannakis G., Spanos L., Cox S., Madeno E., de Pablo B.,
 RA Mcdonnell J., Peter A., Schottler P., Werner M., Mourikioti F.,
 RA Beinert N., Dowe G., Schaefer U., Jacek H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamitso A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valanti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RL melanogaster.";
 RL Science 287:2220-2222(2000).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L22e family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 DR EMBL, U2587; AAB17433.1; -
 DR EMBL, AF003418; AAF45546.1; -
 DR EMBL, AL132792; CAB60023.1; -
 DR Inctact; P50887; -
 DR FlyBase; FBgn0015288; RpL22.
 DR InterPro; IPR002671; Ribosomal_L22e.
 DR Pfam; PF01776; Ribosomal_L22e; 1.
 DR ProDom; PD007306; Ribosomal_L22e; 1.
 KW Ribosomal protein.
 FT DOMAIN 24 31 Poly-Ala.
 FT DOMAIN 46 50 Poly-Ala.
 FT DOMAIN 65 78 Poly-Ala.
 FT DOMAIN 93 90 Poly-Ala.
 FT DOMAIN 103 112 Poly-Ala.
 FT DOMAIN 136 152 Poly-Ala.
 FT DOMAIN 185 188 Poly-Lys.
 FT DOMAIN 292 299 Poly-Lys.
 SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;
 Query Match 64.9%; Score 48; DB 1; Length 299;
 Best Local Similarity 73.3%; Pred. No. 10;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EKPKVEAYKAAAPA 15
 DB 36 EKPKAEAKKPAAPAA 50
 RESULT 3
 ID Q9UN1 PRELIMINARY; PRT; 312 AA.
 AC Q9UN1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein L22 (Fragment).
 GN Name=RpL22; Synonyms=rpL22;
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99133206; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
 RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;
 RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal
 RT proteins, L22 and L23a, with unique histone-like amino-terminal
 RT extensions.";
 RL Gene 226:339-345(1999).
 DR EMBL, AF080131; AAD19341.1; -
 DR FlyBase; FBgn0015288; RpL22.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro: IPR002671; Ribosomal_L22e.
 DR Pfam: PF01776; Ribosomal_L22e; 1.
 KM Ribosomal protein.
 FT NON_TER
 SO SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
 Query Match 64.9%; Score 48; DB 2; Length 312;
 Best Local Similarity 73.3%; Pred. No. 11;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKVAYKAAAPAA 15
 |||||
 49 EKPKVAYKAAAPAA 63

RESULT 4
 ID Q9AAC8 PRELIMINARY; PRT; 389 AA.
 AC Q9AAC8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein CC0674.
 GN OrderedLocustNames=CC0674;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteriaceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19069 / CB15;
 RX MEDLINE=21073698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nielsen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eissen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
 RA Berry K.J., Uitterlinden T.R., Tran K., Wolf A.M., Vamathavan J.J.,
 RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
 RA Fraser C.M.;
 RL "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4116-4141(2001).
 DR EMBL: AEO05743; AAK22659.1; -.
 DR PIR: G87332; G87332.
 DR TIGR: CC0674; -.
 DR InterPro: IPR008262; Lipase_AS.
 DR InterPro: IPR00897; SRP54.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
 DR PROSITE: PS00300; SRP54; UNKNOWN_1.
 KM Complete proteome; Hypothetical protein.
 SO SEQUENCE 389 AA; 40769 MW; C6DD05B8CEBD150E CRC64;
 Query Match 64.9%; Score 48; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 13;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKVAYKAAAPAA 15
 |||||
 66 KTSVETFKAAAPAA 79

RESULT 5
 ID Q7SDS7 PRELIMINARY; PRT; 458 AA.
 AC Q7SDS7;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU03083.1;
 OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
 RA Elting T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Seitzemerkhoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
 RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamvesellis M., Manceill E., Bielke C., Rudd S., Friseman D.,
 RA Krysstofowa S., Rasmussen C., Metzgerberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman I.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbote D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.;
 RL "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABX0100044; EAA34940.1; -.
 SO SEQUENCE 458 AA; 49949 MW; 196D609BF9320496 CRC64;
 Query Match 63.5%; Score 47; DB 2; Length 458;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVAYKAAAPAA 15
 |||||
 78 QPKQXAKAAAPAA 92

RESULT 6
 ID Q7NVT5 PRELIMINARY; PRT; 555 AA.
 AC Q7NVT5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=CV2257;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida F.,
 RA Alves-Gomes J.A., Andrade E.M., Aratipe J., de Araujo M.F.R.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Batous L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burly H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chneire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzielli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Gratiapaglia D., Grissard E.C., Hama E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Mantio G.P., Marinho A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolais M.F., Oliveira J.G., Oliveira S.C.,
 RA Patxao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,

RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Sena H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens W.B.R., Steindel M., Teixeira S.R., Umenyi T.,
 RA Vettore A., Wasseem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 DR EMBL: A6016918; AAC59929.1;
 DR InterPro: IPR005475; Transketolase_CR.
 DR InterPro: IPR005474; Transketolase_N.
 DR InterPro: IPR009014; Transketolase_C like.
 DR Pfam: PF00456; Transketolase_N; 1.
 DR Pfam: PF02779; Transket. pyr; 1.
 KM Complete proteome, Hypothetical protein.
 SQ SEQUENCE 555 AA; 60134 MW; AD1IDEC79CA3BEO1 CRC64;

Query Match 62.2%; Score 46; DB 2; Length 555;
 Best Local Similarity 57.1%; Pred. No. 39;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKVAYKAAAP 14
 DB 526 EMPRIETFOAAAP 539

RESULT 7
 Q7S9W8 PRELIMINARY; PRT; 1923 AA.
 ID Q7S9W8; PRELIMINARY; PRT; 1923 AA.
 AC Q7S9W8;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU06338.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR744;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Jakins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selkirk C.P., Kinsey U.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothne G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thoman N., Barrett R., Greer S.,
 RA Kamal M., Kamysaselis M., Mauceli B., Bielke C., Rudd S., Frisman D.,
 RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
 RA Desouza C.C., Glass J., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Nativig D.O., Alex L.A., Manhaupt G., Ebbold D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 CC -1- FUNCTION: Control of topological states of DNA by transient
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
 CC makes double-strand breaks (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data
 DR EMBL: AABX01000209; EAA31136.1; .

DR HSP: P06766; 1BJT.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO: GO:0006265; P:DNA topological change; IEA.
 DR InterPro: IPR003594; ATPbind ATPase.
 DR InterPro: IPR003957; CRA_NFYB_topis.
 DR InterPro: IPR015558; DNA_gyrase_B.
 DR InterPro: IPR001241; DNA_topoisolt.
 DR InterPro: IPR002205; DNA_topoisolv.
 DR Pfam: PF00204; DNA_gyraseB; 1.
 DR Pfam: PF00521; DNA_topoisolv; 1.
 DR Pfam: PF02518; HATPase c; 1.
 DR PRINTS: PR00615; CCAATSUBUNTA.
 DR PRINTS: PR00418; TP12FAMILY.
 DR ProDom: PD149633; DNA_gyrase_B; 1.
 DR ProDom: PD000742; DNA_topoisolv; 1.
 DR PROSITE: PS00177; TOPOISOMERASE II; UNKNOWN 1.
 KM ATP-binding; DNA-binding; Hypothetical protein; Isomerase;
 KW Topoisomerase.
 SQ SEQUENCE 1923 AA; 213143 MW; 1063EAE1ED142E0 CRC64;

Query Match 62.2%; Score 46; DB 2; Length 1923;
 Best Local Similarity 78.6%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKVAYKAAAPA 15
 DB 1799 KPKVAYKAAAPA 1812

RESULT 8
 MEF_MOUSE
 ID MEF_MOUSE STANDARD; PRT; 192 AA.
 AC P09541;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Myosin light chain 1, atrial/fetal isoform (MLC1A) (MLC1EMB).
 GN Name=MLC1a; Synonyms=My1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RA MEDLINE=88315068; PubMed=2842339;
 RA Barton P.J.R., Robert B., Cohen A., Garner I., Saason D., Weydert A.,
 RA Buckingham M.E.;
 RT "Structure and sequence of the myosin alkali light chain gene
 RT expressed in adult cardiac atria and fetal striated muscle.";
 RL J. Biol. Chem. 263:12669-12676(1988).
 RN [2]
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN=C3H;
 RA MEDLINE=89057447; PubMed=3194193;
 RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
 RA Buckingham M.E.;
 RT "Promoter analysis of myosin alkali light chain genes expressed in
 RT mouse striated muscle.";
 RL Nucleic Acids Res. 16:10037-10052(1988).
 CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
 CC chains.
 CC -1- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal
 CC skeletal and ventricular muscle.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
 CC PROTEIN DOES NOT BIND CALCIUM.
 CC -----
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DR EMBL; M20772; AAA39721.1; JOINED.
DR EMBL; M31017; AAA39721.1; JOINED.
DR EMBL; M20769; AAA39721.1; JOINED.
DR EMBL; M20770; AAA39721.1; JOINED.
DR EMBL; M20771; AAA39721.1; JOINED.
DR EMBL; X13971; CA331414.1; JOINED.
DR EMBL; M19436; AAA39720.1; JOINED.
DR PIR; A31114; MOMS4E.
DR HSSP; P02607; IBR1.
DR MGD; MGI:97267; Myla.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand.
DR ProDom; PD000012; EF-hand; 2.
KW Multigene family; Muscle protein; Myosin.
FT INIT MET 0
SQ SEQUENCE 192 AA; 21028 MW; B0439D512FA19C38 CRC64;

Query Match 60.8%; Score 45; DB 1; Length 192;
Best Local Similarity 71.4%; Pred. No. 22;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KPKVEAYKAAAPA 15
Db 6 EPKKEAKKPAAPA 19

RESULT 9

Q6YSU4 PRELIMINARY; PRT; 299 AA.
AC Q6YSU4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0680C01.22.
GN Name=P0680C01.22;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nupponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0680C01."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006344; BAC84796.1; -.
KW Hypothetical protein.
SQ SEQUENCE 299 AA; 31850 MW; 4C14C4070BC31552 CRC64;

Query Match 60.8%; Score 45; DB 2; Length 299;
Best Local Similarity 73.3%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKPRVEAYKAAAPA 15
Db 262 EAPRVEATPAAATA 276

RESULT 10

Q92TW2 PRELIMINARY; PRT; 306 AA.
AC Q92TW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Smb20676.
GN ORFNames=Smb20676;
OS Rhizobium meliloti (Sinorhizobium meliloti).

OG Plasmid pSymB.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=11396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Flann T.M., Weidner S., Wong K., Buhrmaster J., Chain P.,
Vornolter F.J., Hernandez-Lucas I., Becker A., Cowie A., Guzy J.,
Goldberg B., Puchler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL591985; CAC49783.1; -.
DR PIR; G96014; G96014.
DR InterPro; IPR009273; DUF930.
DR Pfam; PF06059; DUF930; 1.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 306 AA; 32638 MW; 01D9CC644001E67E CRC64;

Query Match 60.8%; Score 45; DB 2; Length 306;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPKVEAYKAAAPA 15
Db 6 RPOEAPESAAAPA 79

RESULT 11

Q869Y7 PRELIMINARY; PRT; 439 AA.
AC Q869Y7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
DE dihydrolipoamide succinyltransferase component of 2-oxoglutarate
dehydrogenase complex, mitochondrial (EC 2.3.1.61) (E2) (E2K).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szatranek K., Pachepat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
DR EMBL; AC116305; AA052267.1; -.
DR HSSP; P07016; 1CAT.
DR GO; GO:0045352; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acylttransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransferase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR001053; Hybrid_motif.
DR InterPro; IPR003016; Lipoyl_BS.
DR InterPro; IPR006255; SuctB.
DR Pfam; PF00198; 2-oxoacid_dh; 1.

Query Match 59.5%; Score 44; DB 1; Length 238;
 Best Local Similarity 64.3%; Pred. No. 40;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15
 |||||
 200 KPAPAYQAPAPAPA 213

RESULT 14

ID 062176 PRELIMINARY; PRT; 342 AA.

AC 062176;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DE Phosphate ABC transporter, periplasmic phosphate-binding protein.
 GN Name=pts; ORFNames=BMA0780;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;

RA Nieman W.C., Deshazer D., Kim H.S., Tettein H., Nelson K.E.,
 RA Feldblyum T., Ulrich R.L., Roming C.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dmitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarría S.,
 RA Selengut J., Shambhlin C., Sullivan S.A., White O., Xu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the Burkholderia mallei genome";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000010; AAU49558.1; -
 SO SEQUENCE 342 AA; 36156 MW; E425E7A18B262B27 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 342;
 Best Local Similarity 64.3%; Pred. No. 55;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15
 :|||:|||||
 Db 238 EPKTEFKAAAGA 251

RESULT 15

ID 063V82 PRELIMINARY; PRT; 342 AA.

AC 063V82;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Phosphate transport system, substrate-binding exported periplasmic
 protein.
 GN Name=pts; Synonyms=phos; ORFNames=BP5L1359;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX PubMed=15377794;

RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebaihia M., Thomson N.R., Bacon N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
 RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitch E., Rutherford K., Sanders M., Simmonds M.,

RA Songsiivilai S., Stevens K., Tumapa S., Veearatchaveest M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Burkholderia pseudomallei";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571965; CAH35357.1; -
 SO SEQUENCE 342 AA; 36156 MW; E425E7A18B262B27 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 342;
 Best Local Similarity 64.3%; Pred. No. 55;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15
 :|||:|||||
 Db 238 EPKTEFKAAAGA 251

Search completed: February 26, 2005, 23:55:44
 Job time : 66.2041 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 76.6837 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583A-86
Perfect score: 76
Sequence: 1 EAPKYEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1980s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	100.0	15	5	ABP52290	ABP52290 HLA-DR2 m
2	76	100.0	15	5	ABP52292	ABP52292 HLA-DR2 m
3	72	94.7	15	5	ABP52304	ABP52304 HLA-DR2 m
4	71	93.4	15	5	ABP52291	ABP52291 HLA-DR2 m
5	68	89.5	15	5	ABP52305	ABP52305 HLA-DR2 m
6	67	88.2	15	5	ABP52297	ABP52297 HLA-DR2 m
7	66	86.8	15	5	ABP52289	ABP52289 HLA-DR2 m
8	63	82.9	15	5	ABP52299	ABP52299 HLA-DR2 m
9	60	78.9	15	5	ABP52270	ABP52270 HLA-DR2 m
10	60	78.9	15	5	ABP52272	ABP52272 HLA-DR2 m
11	59	77.6	17	5	ABP52303	ABP52303 HLA-DR2 m
12	58	76.3	15	5	ABP52300	ABP52300 HLA-DR2 m
13	55	72.4	15	5	ABP52271	ABP52271 HLA-DR2 m
14	55	72.4	15	5	ABP52298	ABP52298 HLA-DR2 m
15	55	72.4	17	5	ABP52294	ABP52294 HLA-DR2 m
16	55	72.4	17	5	ABP52296	ABP52296 HLA-DR2 m
17	55	72.4	17	5	ABP52302	ABP52302 HLA-DR2 m
18	55	72.4	19	5	ABP52295	ABP52295 HLA-DR2 m
19	54	71.1	15	5	ABP52267	ABP52267 HLA-DR2 m
20	54	71.1	15	5	ABP52257	ABP52257 HLA-DR2 m
21	52	68.4	15	5	ABP52293	ABP52293 HLA-DR2 m
22	50	65.8	15	5	ABP52261	ABP52261 HLA-DR2 m
23	50	65.8	15	5	ABP52269	ABP52269 HLA-DR2 m
24	50	65.8	15	5	ABP52268	ABP52268 HLA-DR2 m
25	49	64.5	15	5	ABP52265	ABP52265 HLA-DR2 m

26	49	64.5	15	5	ABP52240	ABP52240 HLA-DR2 m
27	49	64.5	15	5	ABP52241	ABP52241 HLA-DR2 m
28	49	64.5	15	5	ABP52249	ABP52249 HLA-DR2 m
29	49	64.5	15	5	ABP52263	ABP52263 HLA-DR2 m
30	48	63.2	15	5	ABP52243	ABP52243 HLA-DR2 m
31	48	63.2	15	5	ABP52258	ABP52258 HLA-DR2 m
32	48	63.2	15	5	ABP52260	ABP52260 HLA-DR2 m
33	47	61.8	15	5	ABP52301	ABP52301 HLA-DR2 m
34	47	61.8	105	4	ABP52293	ABP52293 HLA-DR2 m
35	47	61.8	781	8	ADN60395	ADN60395 B. lichen
36	47	61.8	781	8	ADN60505	ADN60505 B. lichen
37	47	61.8	781	8	ADN60519	ADN60519 B. lichen
38	46	60.5	15	5	ABP52255	ABP52255 HLA-DR2 m
39	46	60.5	15	5	ABP52251	ABP52251 HLA-DR2 m
40	46	60.5	15	5	ABP52239	ABP52239 HLA-DR2 m
41	46	60.5	99	4	ABP52290	ABP52290 Drosophila
42	45.5	59.9	815	5	AD193027	AD193027 Thermus s
43	45.5	59.9	815	5	AD193029	AD193029 Thermus s
44	45.5	59.9	831	5	AD193037	AD193037 Thermus s
45	45.5	59.9	838	5	AD192947	AD192947 Construct

ALIGNMENTS

RESULT 1
ABP52290
ID ABP52290 standard; peptide; 15 AA.
XX AC ABP52290;
XX DT 16-OCT-2002 (first entry)
DE HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
XX PN 01-AUG-2002.
XX PD 24-JAN-2002; 2002WO-US002071.
XX PF 24-JAN-2001; 2001US-0263569P.
XX PR (HARD) HARVARD COLLEGE.
XX PA Strominger JL, Fridakis-Hareli M;
PI WPI; 2002-608439/65.
XX DR
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agent. The peptide further inhibits proliferation
CC of autotumour-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EAPKYEAYKAAAPA 15
1 EAPKYEAYKAAAPA 15
DB 1 EAPKYEAYKAAAPA 15
RESULT 2
ABP52292
ID ABP52292 standard; peptide; 15 AA.
XX
AC ABP52292;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
PI Strominger JL, Fridkis-Hareli M;
PI Strominger JL, Fridkis-Hareli M;
PI MPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agent. The peptide further inhibits proliferation
CC of autotumour-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EAPKYEAYKAAAPA 15
1 EAPKYEAYKAAAPA 15
DB 1 EAPKYEAYKAAAPA 15
RESULT 3
ABP52304
ID ABP52304 standard; peptide; 15 AA.
XX
AC ABP52304;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:98.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
PI Strominger JL, Fridkis-Hareli M;
PI Strominger JL, Fridkis-Hareli M;
PI MPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agent. The peptide further inhibits proliferation
CC of autotumour-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 94.7%; Score 72; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EAPKYEAYKAAAPA 15

Db 1 EAPKPEAYKAAAPA 15

RESULT 4

ABP52291 standard; peptide; 15 AA.

AC ABP52291; 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:85.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

OS Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 15 AA;

Query Match 93.4%; Score 71; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAPKPEAYKAAAPA 15
| | | | | | | | | | | | | | | | |
Db 1 EAPKPEAYKAAAPA 15

RESULT 5
ABP52305
ID ABP52305 standard; peptide; 15 AA.

XX ABP52305;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:99.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

OS Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 15 AA;

Query Match 89.5%; Score 68; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAPKPEAYKAAAPA 15
| | | | | | | | | | | | | | | | |
Db 1 EAPKPEAYKAAAPA 15

RESULT 6
ABP52297 standard; peptide; 15 AA.

AC ABP52297;

DE 16-OCT-2002 (first entry)

XX HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX

KM	Human leukocyte antigen, HLA; major histocompatibility complex; MHC;
KM	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM	immune response; antiinflammatory; neuroprotective; proliferation;
KM	MHC class II protein inhibitor; demyelinating disease; inhibition;
KM	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM	anti-tumour necrosis factor agent.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
PF	24-JAN-2002; 2002WO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	Strominger JL, Fridkis-Hareli M;
XX	
DR	WPI; 2002-608439/65.
XX	
PS	Claim 28; Page 39; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	demyelinating condition, and a side effect of administering an anti-
CC	tumour necrosis factor agents. The peptide further inhibits proliferation
CC	of autointerferon-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC	ABP52305 represent peptides used in the exemplification of the present
CC	invention
XX	
XX	
SQ	Sequence 15 AA;
XX	
Query Match	88.2%; Score 67; DB 5; Length 15;
Best local Similarity	86.7%; Pred. No. 0.00026;
Matches 13; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	1 EAPKYEAYKAAAPA 15
Db	1 EKPKFEAYKAAAPA 15
XX	
RESULT 7	
ABP52289	
ID	ABP52289 standard; peptide; 15 AA.
XX	
XX	ABP52289;
XX	
DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:83.
KM	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM	immune response; antiinflammatory; neuroprotective; proliferation;
KM	MHC class II protein inhibitor; demyelinating disease; inhibition;
KM	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM	anti-tumour necrosis factor agent.
XX	

[illegible]

PF 24-JAN-2002; 2002W0-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
PR
XX (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP5305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 82.9%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 EAPKVEAYKAAAPA 15
DB 1 EKPKVEAYKAAAPA 15
RESULT 9
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
XX ABP52270;
XX
DT 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:64.
DE
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX W0200259143-A2.
PN
XX 01-AUG-2002.
PD
XX 24-JAN-2002; 2002W0-US002071.
PF
XX 24-JAN-2001; 2001US-0263569P.
PR
XX (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
PI

XX
DR WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP5305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 78.9%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0039;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 EAPKVEAYKAAAPA 15
DB 1 EKPKVEAYKAAAPA 15
RESULT 10
ABP52272
ID ABP52272 standard; peptide; 15 AA.
XX
XX ABP52272;
XX
DT 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:66.
DE
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX W0200259143-A2.
PN
XX 01-AUG-2002.
PD
XX 24-JAN-2002; 2002W0-US002071.
PF
XX 24-JAN-2001; 2001US-0263569P.
PR
XX (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

XX

XX Query Match 78.9%; Score 60; DB 5; Length 15;

XX Best Local Similarity 86.7%; Pred. No. 0.0039; Mismatches 2; Indels 0; Gaps 0;

XX Matches 13; Conservative 0;

QY 1 EAPKYAVYKAAAPA 15

DB 1 EAKKYEAYKRAAAAA 15

RESULT 11

ABP52303

ID ABP52303 standard; peptide; 17 AA.

XX

XX ABP52303;

XX

XX 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:97.

XX

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KM immune response; antiinflammatory; neuroprotective; proliferation;

KM MHC class II protein inhibitor; demyelinating disease; inhibition;

KM post-viral encephalomyelitis; post-vaccine demyelinating condition;

KM anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

OS

PN WO200259143-A2.

XX

XX 01-AUG-2002.

XX

XX 24-JAN-2002; 2002WO-US002071.

XX

XX 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridakis-Hareli M;

XX

XX WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

XX Claim 28; Page 39; 54pp; English.

XX

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 17 AA;

XX

XX Query Match 77.6%; Score 59; DB 5; Length 17;

XX Best Local Similarity 80.0%; Pred. No. 0.0066; Mismatches 2; Indels 0; Gaps 0;

XX Matches 12; Conservative 1;

QY 1 EAPKYAVYKAAAPA 15

DB 3 EAKKYEAYKRAAAAA 17

RESULT 12

ABP52300

ID ABP52300 standard; peptide; 15 AA.

XX

XX ABP52300;

XX

XX 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:94.

XX

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KM immune response; antiinflammatory; neuroprotective; proliferation;

KM MHC class II protein inhibitor; demyelinating disease; inhibition;

KM post-viral encephalomyelitis; post-vaccine demyelinating condition;

KM anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

OS

PN WO200259143-A2.

XX

XX 01-AUG-2002.

XX

XX 24-JAN-2002; 2002WO-US002071.

XX

XX 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridakis-Hareli M;

XX

XX WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

XX Claim 28; Page 39; 54pp; English.

XX

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 76.3%; Score 58; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0084;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 EAPKYEAYKAAAPAA 15
DB 1 EKPKKEAFKAAAPAA 15
RESULT 13
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002MO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Frickis-Harell M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 72.4%; Score 55; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.027;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 EAPKYEAYKAAAPAA 15
DB 1 EKPKKEAFKAAAPAA 15
RESULT 14
ABP52298
ID ABP52298 standard; peptide; 15 AA.
XX
AC ABP52298;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN MO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002MO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Frickis-Harell M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 72.4%; Score 55; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.027;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 EAPKYEAYKAAAPAA 15
DB 1 EKPKKEAFKAAAPAA 15

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RESULT 15
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 5app; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
XX
Query Match 72.4%; Score 55; DB 5; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAPKYEAYKAAAPA 15
| | | | | | | | | |
Db 3 EKAKYEAYKAAAPA 17

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Search completed: February 26, 2005, 23:48:22
 Job time : 77.6837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 : Search time 20.051 Seconds
(without alignments)
55.844 Million cell updates/sec

Title: US-10-056-583A-86
Perfect score: 76
Sequence: 1 EAPRYEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/BACKFILE1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	55.3	287	3	US-09-105-697-7
2	42	55.3	287	3	US-09-105-697-8
3	42	55.3	288	3	US-09-105-697-3
4	42	55.3	291	3	US-09-105-697-4
5	42	55.3	291	3	US-09-105-697-5
6	42	55.3	291	3	US-09-105-697-6
7	42	55.3	830	1	US-07-977-434-6
8	42	55.3	830	1	US-08-458-819-6
9	42	55.3	830	5	PCT-US91-07035-6
10	42	55.3	831	1	US-08-073-384C-5
11	42	55.3	831	1	US-08-254-359A-5
12	42	55.3	831	1	US-08-483-043-5
13	42	55.3	831	1	US-08-481-238-5
14	42	55.3	831	2	US-08-471-066B-5
15	42	55.3	831	2	US-08-484-956-5
16	42	55.3	831	2	US-08-757-653-5
17	42	55.3	831	2	US-08-599-491-5
18	42	55.3	831	2	US-08-756-386-5
19	42	55.3	831	2	US-08-823-516-5
20	42	55.3	831	3	US-08-682-853A-5
21	42	55.3	831	3	US-08-759-038-5
22	42	55.3	831	3	US-08-758-314-5
23	42	55.3	831	3	US-09-350-309-5
24	42	55.3	831	3	US-08-520-946-5
25	42	55.3	831	4	US-09-684-938-5
26	42	55.3	831	4	US-09-308-825A-5
27	42	55.3	831	4	US-09-758-282B-5

28	42	55.3	831	4	US-09-655-378A-5	Sequence 5, Appli
29	42	55.3	831	4	US-09-940-244-5	Sequence 5, Appli
30	42	55.3	831	4	US-09-333-145-5	Sequence 5, Appli
31	42	55.3	831	4	US-09-577-304A-5	Sequence 5, Appli
32	42	55.3	832	4	US-09-758-282B-251	Sequence 251, App
33	42	55.3	832	4	US-09-758-282B-268	Sequence 268, App
34	42	55.3	832	4	US-09-577-304A-251	Sequence 251, App
35	42	55.3	832	4	US-09-577-304A-268	Sequence 268, App
36	42	55.3	833	1	US-08-073-384C-8	Sequence 8, Appli
37	42	55.3	833	1	US-08-254-359A-8	Sequence 8, Appli
38	42	55.3	833	1	US-08-483-043-8	Sequence 8, Appli
39	42	55.3	833	1	US-08-481-238-8	Sequence 8, Appli
40	42	55.3	833	2	US-08-471-066B-8	Sequence 8, Appli
41	42	55.3	833	2	US-08-484-956-8	Sequence 8, Appli
42	42	55.3	833	2	US-08-757-653-8	Sequence 8, Appli
43	42	55.3	833	2	US-08-599-491-8	Sequence 8, Appli
44	42	55.3	833	2	US-08-756-386-8	Sequence 8, Appli
45	42	55.3	833	2	US-08-823-516-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-105-697-7
Sequence 7, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-7

Query Match 55.3%; Score 42; DB 3; Length 287;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14
Db 75 YEAYKAGRAP 84

RESULT 2
US-09-105-697-8
Sequence 8, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-8
Query Match 55.3%; Score 42; DB 3; Length 287;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 YEAYKAAAP 14
Db 75 YEAYKAGRAP 84
RESULT 3
US-09-105-697-3
Sequence 3, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-3
Query Match 55.3%; Score 42; DB 3; Length 288;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 YEAYKAAAP 14
Db 77 YEAYKAGRAP 86
RESULT 4
US-09-105-697-4
Sequence 4, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-4
Query Match 55.3%; Score 42; DB 3; Length 291;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 YEAYKAAAP 14

Db 79 YEAYKAGRAP 88

RESULT 5

US-09-105-697-5
; Sequence 5, Application US/09105697
; Patent No. 6228628
; GENERAL INFORMATION:
; APPLICANT: Gelfand Ph.D., David H.
; APPLICANT: Reichert, Fred L.
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roche Molecular Systems
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08876
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,697
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry Ph.D., Douglas A.
; REGISTRATION NUMBER: 35321
; REFERENCE/DOCKET NUMBER: 1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-105-697-5

Query Match 55.3%; Score 42; DB 3; Length 291;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAP 14
Db 79 YEAYKAGRAP 88

RESULT 6

US-09-105-697-6
; Sequence 6, Application US/09105697
; Patent No. 6228628
; GENERAL INFORMATION:
; APPLICANT: Gelfand Ph.D., David H.
; APPLICANT: Reichert, Fred L.
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roche Molecular Systems
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08876
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-6

Query Match 55.3%; Score 42; DB 3; Length 291;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAP 14
Db 79 YEAYKAGRAP 88

RESULT 7

US-07-977-434-6
; Sequence 6, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509

;; FILING DATE: 17-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 899,241
;; FILING DATE: 22-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 746,121
;; FILING DATE: 15-AUG-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US90/07641
;; FILING DATE: 21-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 585,471
;; FILING DATE: 20-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 455,611
;; FILING DATE: 22-DEC-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 609,157
;; FILING DATE: 02-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 557,517
;; FILING DATE: 24-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Luann Cseert
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 814-2972
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 830 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-977-434-6

Query Match 55.3%; Score 42; DB 1; Length 830;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14
Db 75 YEAYKAGRAP 84

RESULT 8
US-08-458-819-6
; Sequence 6, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,819
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,434
; FILING DATE: 23-FEB-1993

;; APPLICATION NUMBER: US 590,490
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 590,466
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 590,213
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 523,394
;; FILING DATE: 15-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 143,441
;; FILING DATE: 12-JAN-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 063,509
;; FILING DATE: 17-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 899,241
;; FILING DATE: 22-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 746,121
;; FILING DATE: 15-AUG-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US90/07641
;; FILING DATE: 21-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 585,471
;; FILING DATE: 20-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 455,611
;; FILING DATE: 22-DEC-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 609,157
;; FILING DATE: 02-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 557,517
;; FILING DATE: 24-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Luann Cseert
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 814-2972
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 830 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-458-819-6

Query Match 55.3%; Score 42; DB 1; Length 830;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14
Db 75 YEAYKAGRAP 84

RESULT 9
PCT-US91-07035-6
; Sequence 6, Application PC/TUS9107035
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-359A-5

Query Match 55.3%; Score 42; DB 1; Length 831;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14
DB 77 YEAYKAGRAP 86

RESULT 12
US-08-483-043-5
Sequence 5, Application US/08483043
Patent No. 5691142
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,043
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-043-5

Query Match 55.3%; Score 42; DB 1; Length 831;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14
DB 77 YEAYKAGRAP 86

RESULT 13
US-08-481-238-5
Sequence 5, Application US/08481238
Patent No. 5795763
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,238
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-481-238-5

Query Match 55.3%; Score 42; DB 1; Length 831;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14

Db 77 YEAYKAGRAP 86

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RESULT 14
US-08-471-066B-5
; Sequence 5, Application US/08471066B
; Patent No. 5837450
; GENERAL INFORMATION:
; APPLICANT: Dahlberg, James E.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
; TITLE OF INVENTION: DNA Polymerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,066B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/254,359
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/073,384
; FILING DATE: 04-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/986,330
; FILING DATE: 07-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-01800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-066B-5

Query Match 55.3%; Score 42; DB 2; Length 831;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 5 YEAYKAAAP 14
Db 77 YEAYKAGRAP 86

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RESULT 15
US-08-484-956-5
; Sequence 5, Application US/08484956
; Patent No. 5843654
; GENERAL INFORMATION:
; APPLICANT: DAHLBERG, JAMES E.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: BROW, MARY ANN D.
```

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APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
; TITLE OF INVENTION: DETECTION OF P53 MUTATIONS
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAVESTOCK, MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,956
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,601
; FILING DATE: 09-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,164
; FILING DATE: 09-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/254,359
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,384
; FILING DATE: 04-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/986,330
; FILING DATE: 07-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, J. PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8338
; TELEFAX: (415) 705-8410
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-956-5

Query Match 55.3%; Score 42; DB 2; Length 831;
Best Local Similarity 80.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 5 YEAYKAAAP 14
Db 77 YEAYKAGRAP 86

Search completed: February 26, 2005, 23:59:28
Job time : 21.051 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 53.5714 Seconds
(without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583A-86
Perfect score: 76
Sequence: 1 EAPKRYKAAAPAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
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- 14: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
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- 17: /cgn2_6/prodata/1/pubppaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	15	US-10-056-583-84	Sequence 84, Appl
2	76	100.0	15	US-10-056-583-86	Sequence 86, Appl
3	72	94.7	15	US-10-056-583-88	Sequence 98, Appl
4	71	93.4	15	US-10-056-583-85	Sequence 85, Appl
5	68	89.5	15	US-10-056-583-99	Sequence 99, Appl
6	67	88.2	15	US-10-056-583-91	Sequence 91, Appl
7	66	86.8	15	US-10-056-583-83	Sequence 83, Appl
8	63	82.9	15	US-10-056-583-93	Sequence 93, Appl
9	60	78.9	15	US-10-056-583-64	Sequence 64, Appl
10	60	78.9	15	US-10-056-583-66	Sequence 66, Appl
11	59	77.6	17	US-10-056-583-97	Sequence 97, Appl
12	58	76.3	15	US-10-056-583-94	Sequence 94, Appl
13	55	72.4	15	US-10-056-583-65	Sequence 65, Appl

14	55	72.4	17	US-10-056-583-88	Sequence 88, Appl
15	55	72.4	17	US-10-056-583-90	Sequence 90, Appl
16	55	72.4	17	US-10-056-583-96	Sequence 96, Appl
17	55	72.4	19	US-10-056-583-89	Sequence 89, Appl
18	54	71.1	15	US-10-056-583-51	Sequence 51, Appl
19	54	71.1	15	US-10-056-583-61	Sequence 61, Appl
20	52	68.4	15	US-10-056-583-87	Sequence 87, Appl
21	50	65.8	15	US-10-056-583-85	Sequence 55, Appl
22	50	65.8	15	US-10-056-583-62	Sequence 62, Appl
23	50	65.8	15	US-10-056-583-63	Sequence 63, Appl
24	49	64.5	15	US-10-056-583-34	Sequence 34, Appl
25	49	64.5	15	US-10-056-583-35	Sequence 35, Appl
26	49	64.5	15	US-10-056-583-43	Sequence 43, Appl
27	49	64.5	15	US-10-056-583-57	Sequence 57, Appl
28	49	64.5	15	US-10-056-583-59	Sequence 59, Appl
29	48	63.2	15	US-10-056-583-37	Sequence 37, Appl
30	48	63.2	15	US-10-056-583-52	Sequence 52, Appl
31	48	63.2	15	US-10-056-583-54	Sequence 54, Appl
32	47	61.8	15	US-10-056-583-95	Sequence 95, Appl
33	46	60.5	15	US-10-056-583-33	Sequence 33, Appl
34	46	60.5	15	US-10-056-583-45	Sequence 45, Appl
35	46	60.5	15	US-10-056-583-49	Sequence 49, Appl
36	46	60.5	15	US-10-056-583-92	Sequence 92, Appl
37	45.5	59.9	815	US-09-864-636A-580	Sequence 580, App
38	45.5	59.9	815	US-09-864-636A-582	Sequence 582, App
39	45.5	59.9	815	US-09-864-426A-580	Sequence 580, App
40	45.5	59.9	815	US-09-864-426A-582	Sequence 582, App
41	45.5	59.9	815	US-10-084-839-580	Sequence 580, App
42	45.5	59.9	815	US-10-084-839-582	Sequence 582, App
43	45.5	59.9	815	US-10-084-839-2827	Sequence 2827, App
44	45.5	59.9	815	US-10-084-839-2829	Sequence 2829, App
45	45.5	59.9	831	US-09-864-636A-550	Sequence 590, App

ALIGNMENTS

RESULT 1
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Fridkiss-Harell, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DERMATOLITATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match 100.0%; Score 76; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAPKRYKAAAPAA 15
DB 1 EAPKRYKAAAPAA 15

RESULT 2
US-10-056-583-86

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/ Sequence 86, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 86
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86
```

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Query Match          100.0%; Score 76; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 EAPKVEAYKAAAPA 15
        |||||
Db       1 EAPKVEAYKAAAPA 15
```

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RESULT 3
US-10-056-583-98
/ Sequence 98, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 98
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98
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Query Match          94.7%; Score 72; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EAPKVEAYKAAAPA 15
        |||||
Db       1 EAPKVEAYKAAAPA 15
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RESULT 4
US-10-056-583-85
/ Sequence 85, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
```

```
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 85
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
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Best Local Similarity 93.3%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 EAPKVEAYKAAAPA 15
        |||||
Db       1 EAPKVEAYKAAAPA 15
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```
RESULT 5
US-10-056-583-99
/ Sequence 99, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 99
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
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Best Local Similarity 93.3%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 EAPKVEAYKAAAPA 15
        |||||
Db       1 EAPKVEAYKAAAPA 15
```

```
RESULT 6
US-10-056-583-91
/ Sequence 91, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
```



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; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
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Query Match      88.2%; Score 67; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00026;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 EAPRYEAYKAAAPAA 15
      |||:|||||
Db      1 EKPKFEAYKAAAPAA 15
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```
RESULT 7
US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-83
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Query Match      86.8%; Score 66; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00039;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 EAPRYEAYKAAAPAA 15
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Db      1 EAPYKAYKAAAPAA 15
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RESULT 8
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; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93
```

```
Query Match      82.9%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 EAPRYEAYKAAAPAA 15
      |||:|||||
Db      1 EKPKFEAYKAAAPAA 15
```

```
RESULT 9
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match      78.9%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 EAPRYEAYKAAAPAA 15
      |||:|||||
Db      1 EAAKYEAYKAAAPAA 15
```

```
RESULT 10
US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match 78.9%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 1 EAKKYEAYKAAAPA 15

RESULT 11

US-10-056-583-97
Sequence 97, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match 77.6%; Score 59; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0062;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 3 EAKKYEAYKAAAPA 17

RESULT 12
US-10-056-583-94
Sequence 94, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 94
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94

Query Match 76.3%; Score 58; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.008;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 1 EKPKEBAFKAAAPA 15

RESULT 13
US-10-056-583-65
Sequence 65, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match 72.4%; Score 55; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 1 EAKKYEAYKAAAPA 15

RESULT 14
US-10-056-583-88
Sequence 88, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 88
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match 72.4%; Score 55; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 3 EAKKYEAYKAAAPA 17

RESULT 15

US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridakis-Harell, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match 72.4%; Score 55; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
| | | | | | | | | | | | | | | | |
Db 1 EKAKYEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:22
Job time : 53.5714 secs

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A; Accession: A45943

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <POP>
A/Cross-references: UNIPROT:P13238; GB:M20936; NID:G158728; PID:G158729
C/Genetics:
A:Gene: FlyBase:Vn26Ab
A/Cross-references: FlyBase:FBgn0003980

Query Match 56.3%; Score 43; DB 2; Length 168;
Best Local Similarity 64.3%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAP 15
|||
Db 66 APAQAASAPAP 79

RESULT 3

MOCH4E

myosin alkali light chain 4, embryonic - chicken
N/Alternate names: myosin I23 catalytic light chain

C/Species: Gallus gallus (chicken)
C/Date: 01-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C/Accession: S02065; A29473

R/Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriyama, J. Mol. Biol. 204, 497-505, 1988

A/Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic g

A/Reference number: S02065; MUID:89141751; PMID:3225843

A/Accession: S02065

A:Molecule type: DNA

A:Residues: 1-185 <NAB>

A/Cross-references: UNIPROT:P09540; EMBL:X14428

A/Note: the authors translated the codon CGG for residue 71 as Ala

R/Kawashima, M.; Nabeshima, Y.; Oinata, T.; Fujii-Kuriyama, Y.

J. Biol. Chem. 262, 14408-14414, 1987

A/Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac

A/Reference number: A29473; MUID:88032983; PMID:3667580

A/Accession: A29473

A:Molecule type: mRNA

A:Residues: 1-93; 'L', 95-165; 'L', 167-185 <KAW>

A/Cross-references: GB:J02823; NID:G212339; PION:AAA4957.1; PID:G212340

A/Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1

C/Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac

C/Genetics:

A/Intons: 33/3; 43/1; 93/1; 151/1; 177/1

C/Complex: The myosin molecule contains two heavy chains, two alkali light chains, and t

C/Superfamily: calmodulin; calmodulin repeat homology

C/Keywords: brain; calcium binding; duplication; EF hand; muscle contraction

F/9-73/Domain: calmodulin repeat homology <EF1>

F/118-150/Domain: calmodulin repeat homology <EF3>

F/153-185/Domain: calmodulin repeat homology <EF4>

Query Match

Best Local Similarity 55.3%; Score 42; DB 1; Length 185;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAP 14
|||
Db 8 PKDKAAKAAAP 19

RESULT 4

I50145

homeotic protein Hox M - chicken

N/Alternate names: CHOX M

C/Species: Gallus gallus (chicken)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

C/Accession: I50145; S14512

R/Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.

Leukemia 5, 357-360, 1991

A/Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vltm

A/Reference number: I50145; MUID:91238215; PMID:1674560

A/Accession: I50145

A>Status: preliminary; translated from GB/EMBL/DDBI

A:Molecule type: mRNA

A:Residues: 1-188 <CRO>

A/Cross-references: UNIPROT:P23459; EMBL:X57158; NID:962700; PION:CAA40445.1; PID:96270

C/Genetics:

A:Gene: CHOX M

C/Superfamily: homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/96-152/Domain: homeobox homology <HOX>

Query Match 55.3%; Score 42; DB 2; Length 188;

Best Local Similarity 69.2%; Pred. No. 10;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAP 15
|||
Db 8 PLYSKYKAAAAA 20

RESULT 5

S28845

myosin regulatory light chain LC25, muscle - earthworm (lumbicus terrestris)

C/Species: Lumbricus terrestris (common earthworm)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S28845

R/Serwe, M.; Meyer, H.E.; Craig, A.G.; Carlhoff, D.; d'Haese, J.

Bur. J. Biochem. 211, 341-346, 1993

A/Title: Complete amino acid sequence of the regulatory light chain of obliquely striat

A/Reference number: S28845; MUID:93145966; PMID:8425543

A/Accession: S28845

A:Molecule type: protein

A/Status: preliminary

A/Residues: 1195 <SER>

A/Cross-references: UNIPROT:P80164

C/Superfamily: calmodulin; calmodulin repeat homology

C/Keywords: EF hand

F/55-87/Domain: calmodulin repeat homology <EF1>

Query Match 55.3%; Score 42; DB 2; Length 195;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAP 15
|||
Db 16 DAPAEAPAAAAAP 30

RESULT 6

homeotic protein Hox D8 - mouse

N/Alternate names: homeotic protein Hox 4.3

C/Species: Mus musculus (house mouse)

C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C/Accession: A43562

R/Zipisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Duboi

Development 110, 733-745, 1990

A/Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob

A/Reference number: A43562; MUID:91209232; PMID:1982431

A/Accession: A43562

A:Molecule type: DNA

A/Status: preliminary; not compared with conceptual translation

A/Residues: 1-289 <IZP>

A/Cross-references: UNIPROT:P23463

C/Superfamily: homeotic protein Hox A7; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/196-252/Domain: homeobox homology <HOX>

Query Match 55.3%; Score 42; DB 2; Length 289;

Best Local Similarity 69.2%; Pred. No. 16;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAP 15
|||

Db 8 PLYSKYKAAAAA 20

RESULT 7

G96014
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C/Accession: G96014

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhremeister, J.; Chain, P.; Vorholter, F.J.; Hernat
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: G96014

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-306 <KUR>

A/Cross-references: UNIPROT:Q92TW2; GB:A591985; PIDN:CAC49783.1; PID:G15141270; GSPDB:C

A/Experimental source: strain 1021, megaplasmid pSymB

R/Gilbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Jäme, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: SMD2067d

A/Genome: plasmid

Query Match

Best Local Similarity 55.3%; Score 42; DB 2; Length 306;
Pred. No. 17;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 PKYAYKAAAPA 15

Db 67 PDEAPESAAAPA 79

RESULT 8

E87463

hypothetical protein CC1729 [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C/Accession: E87463

R/Nerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; MUID:21173698; PMID:11259647

A/Accession: E87463

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-428 <STO>

A/Cross-references: UNIPROT:Q9A7J4; GB:A5005673; NID:G13423147; PIDN:AAK23705.1; GSPDB:C

C/Genetics:

A/Gene: CC1729

C/Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match

Best Local Similarity 55.3%; Score 42; DB 2; Length 428;
Pred. No. 24;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 APKYAYKAAA 13

Db 87 APKYAYKAAA 98

RESULT 9

S26675

DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus

C/Species: Thermus aquaticus

C/Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999

C/Accession: S26675; S24929

R/Akhmetzjanov, A.A.; Vakhitov, V.A.

Nucleic Acids Res. 20, 5839, 1992

A/Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from Ther.

A/Reference number: S26675; MUID:93087201; PMID:1454544

A/Accession: S26675

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-831 <AGH>

A/Cross-references: EMBL:X66105; NID:G48165; PIDN:CAA46900.1; PID:G48166

A/Note: the source is designated as Thermus flavus

C/Genetics:

A/Gene: polI

C/Superfamily: DNA-directed DNA polymerase I

C/Keywords: DNA binding; nucleotidyltransferase

Query Match

Best Local Similarity 55.3%; Score 42; DB 2; Length 831;
Pred. No. 45;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAP 14

Db 77 YEAYKAGRAP 86

RESULT 10

A23253

myosin A1 catalytic light chain, skeletal muscle - mouse

C/Species: Mus musculus (house mouse)

C/Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 13-Aug-1999

C/Accession: A23253; S02259

R/Robert, B.; Daubae, P.; Akimenko, M.A.; Cohen, A.; Garner, I.; Guenet, J.L.; Buckingh

Cell 39, 129-140, 1984

A/Title: A single locus in the mouse encodes both myosin light chains 1 and 3, a second

A/Reference number: A90854; MUID:85024885; PMID:6091905

A/Accession: A23253

A/Molecule type: DNA

A/Residues: 1-188 <ROB>

A/Note: the authors translated the codon ATT for residue 173 as Asn

R/Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.

Nucleic Acids Res. 16, 10037-10052, 1988

A/Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striat

A/Reference number: S01944; MUID:89057447; PMID:3194193

A/Accession: S02259

A/Molecule type: DNA

A/Residues: 1-38 <COH>

A/Cross-references: EMBL:X12973; NID:G53140; PIDN:CAA31416.1; PID:G53141

C/Genetics:

A/Intons: 38/3; 48/1; 96/1; 154/1; 180/1

C/Superfamily: calmodulin; calmodulin repeat homology

C/Keywords: alternative splicing; calcium binding; EF hand; muscle; skeletal muscle

F/44-76/Domain: calmodulin repeat homology <EF1>

F/121-153/Domain: calmodulin repeat homology <EF2>

Query Match 53.9%; Score 41; DB 2; Length 188;

Best Local Similarity 64.3%; Pred. No. 15;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 APKYAYKAAADA 15

Db 2 APKYAYKAAADA 15

RESULT 11

M074E

myosin alkali light chain 4, embryonic and atrial - rat

N/Alternate names: MLC4; MLC4b; myosin II catalytic light chain, atrial

C/Species: Rattus norvegicus (Norway rat)

C/Date: 29-Jan-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C/Accession: S09236
 R/Rover, A.S.; McNally, E.M.; Ieinward, L.A.
 Nucleic Acids Res. 18, 1581-1586, 1990
 A/Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expression
 A/Reference number: S09236; MUID:90221887; PMID:2326197
 A/Accession: S09236
 A/Molecule type: mRNA
 A/Residues: 1-193 <ROV>
 A/Cross-references: UNIPROT:P17209; EMBL:X51531; NID:957512; PIDN:CAA35911.1; PID:957513
 C/Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fetal C/Superfamily: calmodulin; calmodulin repeat homology
 C/Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract
 F/47-81/Domain: calmodulin repeat homology <EF1>
 F/126-158/Domain: calmodulin repeat homology <EF3>
 F/161-193/Domain: calmodulin repeat homology <EF4>

Query Match 53.9%; Score 41; DB 1; Length 193;
 Best Local Similarity 69.2%; Pred. No. 16;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PKXEAYKAAAPA 15
 DB 8 PKXEAYKAAAPA 20

RESULT 12
 T51222
 hypothetical protein B24M22.180 [imported] - Neurospora crassa
 C/Species: Neurospora crassa
 C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
 C/Accession: T51222
 R/Schulte, U.; Aign, V.; Hehse, J.; Brandt, P.; Fattmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
 A/Reference number: Z25286
 A/Accession: T51222
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-261 <SCH>
 A/Cross-references: UNIPROT:Q9P390; EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.180
 A/Experimental source: strain OR74A
 C/Genetics:
 A/Gene: NCSP:B24M22.180
 A/Map position: 6
 A/Intons: 250/1

Query Match 53.9%; Score 41; DB 2; Length 261;
 Best Local Similarity 71.4%; Pred. No. 21;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAPA 15
 DB 116 APKYEAYKAAAPA 129

RESULT 13
 B81081
 tryptophan-tryptophan synthetase NMB1471 [imported] - Neisseria meningitidis (strain MC58 se
 C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: B81081
 R/Fetellin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eissen, J.A.
 Hickey, E.K.; Hatt, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 et al.; H.; Qin, H.; Vanathavan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
 Science 287, 1809-1815, 2000
 A/Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A/Reference number: AB1000; MUID:20175755; PMID:10710307
 A/Accession: B81081
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-336 <TET>
 A/Cross-references: UNIPROT:Q9UY09; GB:AE002496; GB:AE002098; NID:97226701; PIDN:AAF4182
 A/Experimental source: serogroup B, strain MC58

C/Genetics:
 A/Gene: NMB1471
 C/Superfamily: tryptophan-tryptophan synthetase

Query Match 53.9%; Score 41; DB 2; Length 336;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
 DB 243 EAPKYEAYKAAAPA 257

RESULT 14
 E81863
 tryptophan-tryptophan synthetase (EC 6.1.1.2) NMA1682 [imported] - Neisseria meningitidis (strain
 C/Species: Neisseria meningitidis
 C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C/Accession: E81863
 R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagers, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A/Reference number: AB1775; MUID:20222556; PMID:10761919
 A/Accession: E81863
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-336 <PAR>
 A/Cross-references: UNIPROT:Q9UY09; GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB8491
 A/Experimental source: serogroup A, strain Z2491
 C/Genetics:
 A/Gene: trps; NMA1682
 C/Superfamily: tryptophan-tryptophan synthetase
 C/Keywords: ligase

Query Match 53.9%; Score 41; DB 2; Length 336;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
 DB 243 EAPKYEAYKAAAPA 257

RESULT 15
 AB3359
 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) [imported] - Brucella melitensis (str
 C/Species: Brucella melitensis
 C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C/Accession: AB3359
 R/Delvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes-
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A/Reference number: AD3252; PMID:11756688
 A/Accession: AB3359
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-447 <KUR>
 A/Cross-references: UNIPROT:O8YH5; GB:AE008917; PIDN:AAL52037.1; PID:gl7982803; GSPDB:
 A/Experimental source: strain 16M
 C/Genetics:
 A/Gene: BME10856
 A/Map position: 1
 C/Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
 C/Keywords: acyltransferase; coenzyme A

Query Match 53.3%; Score 40.5; DB 2; Length 447;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

QY 1 EAPKYEAYKAAAPA 15

Db 98 EAPKDEPKPAKKEAAPA 117

Search completed: February 26, 2005, 23:57:14
Job time : 15.3163 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 65.2041 Seconds
(without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583A-86
Perfect score: 76
Sequence: 1 EAPRYEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	61.8	105	2 Q9FV5	Q9FV5 artichobact
2	47	61.8	294	2 Q93HV7	Q93HV7 bacillus li
3	47	61.8	781	2 Q65UC3	Q65UC3 bacillus li
4	46	60.5	99	2 Q9FV6	Q9FV6 artichobact
5	45	59.2	299	2 Q6YSU4	Q6YSU4 oryza sativ
6	45	59.2	408	2 Q7S7R7	Q7S7R7 neurospora
7	44	57.9	192	1 MLEF MOUSE	P09541 mus musculu
8	44	57.9	316	2 Q6C9T2	Q6C9T2 yarrowia li
9	44	57.9	424	2 Q73BN9	Q73BN9 bacillus ce
10	44	57.9	439	2 Q669Y7	Q669Y7 dictyosteli
11	44	57.9	591	2 Q7WJF6	Q7WJF6 bordetella
12	44	57.9	802	2 Q8H1Y7	Q8H1Y7 hordeum vul
13	44	57.9	802	2 Q8H1Y8	Q8H1Y8 hordeum vul
14	43.5	57.2	277	1 R53 STROCO	Q910d4 streptomyc
15	43	56.6	163	2 Q6JRS4	Q6JRS4 equus cabal
16	43	56.6	168	1 VTU2_DROME	VTU2_DROME
17	43	56.6	380	2 Q7PFG4	Q7PFG4 anopheles g
18	43	56.6	608	2 Q87T98	Q87T98 vibrio para
19	43	56.6	612	2 Q926I4	Q926I4 streptomyc
20	42	55.3	98	2 Q91RI4	Q91RI4 psidium sativ
21	42	55.3	185	1 MLEF CHICK	MLEF CHICK
22	42	55.3	188	1 HXD8_CHICK	HXD8_CHICK
23	42	55.3	195	1 MLEF CHICK	MLEF CHICK
24	42	55.3	289	1 HXD8_MOUSE	HXD8_MOUSE
25	42	55.3	289	2 Q81XZ1	Q81XZ1 mus musculu
26	42	55.3	290	1 HXD8_HUMAN	HXD8_HUMAN
27	42	55.3	306	2 Q92TW2	Q92TW2 homo sapien
28	42	55.3	356	2 Q6K4G2	Q6K4G2 oryza sativ
29	42	55.3	428	2 Q9A7U4	Q9A7U4 cauliobacter
30	42	55.3	458	2 Q7SDS7	Q7SDS7 neurospora
31	42	55.3	548	2 Q87VD3	Q87VD3 pseudomonas

32	42	55.3	555	2 Q7NVT5	Q7NVT5 chromobacte
33	42	55.3	831	1 DPOT_THETH	P30133 thermus the
34	42	55.3	833	1 DPOT_THETH	O52225 thermus the
35	42	55.3	833	2 Q6X9E2	Q6X9E2 thermus fil
36	42	55.3	834	1 DPOT_THETH	P80194 thermus cal
37	42	55.3	834	1 DPOT_THETH	P52028 thermus cal
38	42	55.3	834	2 Q7JUS8	Q7JUS8 thermus the
39	42	55.3	947	2 Q87YI0	Q87YI0 pseudomonas
40	41.5	54.6	214	2 Q88LD7	Q88LD7 pseudomonas
41	41.5	54.6	299	1 RL22_DROME	P50887 drosophila
42	41.5	54.6	312	2 Q9UANI	Q9UANI drosophila
43	41	53.9	121	2 Q8LH24	Q8LH24 oryza sativ
44	41	53.9	121	2 Q8LH24	Q8LH24 oryza sativ
45	41	53.9	187	1 MLEF_MOUSE	P05977 mus musculu

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	105 AA.
Q9FV5	Q9FV5		
AC	Q9FV5		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	CG14377-PA		
CN	ORFNames=CG14377;		
OS	Drosophila melanogaster (fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabler G.L.,		
RA	Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brinkstein P., Brotlier P.,		
RA	Burtis K.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Dutler K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fowler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,		
RA	Glodes A.A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,		
RA	Jatani M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Pacib J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Sprent E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,		
RA	Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,		
RA	Yeh R.F., Zaveri U.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of Drosophila melanogaster."		

```

RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frishe E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Peckol J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weissrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frishe E., Wheeler D.A., Lewis S.E., Rubin J.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tuzy J.L., Whittied E.J., Bayraktaroglu L., Betman B.F.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO03700; AAF5494.1; -
RX FlyBase; FBgn0038148; CG14377.
SQ SEQUENCE 105 AA; 10570 MW; BCE05E9DDBE35C5C CRC64;

Query Match 61.8%; Score 47; DB 2; Length 105;
Best Local Similarity 64.3%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAPA 15
DB 47 APSYSTYAAAAYPA 60

RESULT 2
O93HV7 PRELIMINARY; PRT; 294 AA.
AC O93HV7;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Probable dihydrolipoamide acyltransferase (Fragment).
OS Arthrobacter globiformis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Arthrobacter.
OX NCBI_Taxid=1665;
RN [1]
RP SEQUENCE FROM N.A.
RA Hata H., Oshima Y., Ono K., Mori T., Kochi H.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 lipoyl-binding domains.

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DR EMBL; AB056512; BAB64317.1; -
DR HGSP; P11961; 1LAB.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; F:metabolism; IEA.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3 binding.
DR InterPro; IPR011053; Hybrid_motif.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00364; Biotin_lipoyl; 2.
DR Pfam; PF02817; E3 binding; 1.
DR PROSITE; PS00189; Lipoyl; 2.
KW Acyltransferase; Lipoyl; Transferase.
FT NON TER 294
SQ SEQUENCE 294 AA; 29117 MW; 82C80DE67E48B2B5 CRC64;

Query Match 61.8%; Score 47; DB 2; Length 294;
Best Local Similarity 73.3%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 225 EAPKEAYKAAAPA 239

RESULT 3
O65JG3 PRELIMINARY; PRT; 781 AA.
AC O65JG3;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE SpoIIIE (DNA translocase)
GN Name=spoIIIE; ORFName=BL01204, BL101906;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_Taxid=279010;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential."
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.T., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species."
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AEO17333; AAU04801.1; -
DR EMBL; CP000002; AAU23441.1; -
SQ SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;

Query Match 61.8%; Score 47; DB 2; Length 781;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
DB 264 EKPQAYKAAAPA 278

RESULT 4

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ID	Q9VFW6	PRELIMINARY;	PRT;	99 AA.
AC	Q9VFW6			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)			
DE	CG14374-PA.			
GN	ORFNames=CG14374;			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,			
RA	Abrial J.F., Agbayan A., An H.J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Baau A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,			
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,			
RA	Hosotin D., Houston K.A., Howland T.J., Mei M.H., Ileguam C.,			
RA	Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Laeko P., Lei Y., Levitsky A.A., Li Y., Li Z., Liang Y., Lin X.,			
RA	Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stepleton M., Strong R., Sun E.,			
RA	Svirskaas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,			
RA	Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,			
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	"The genome sequence of <i>Drosophila melanogaster</i> .";			
RL	Science 287:2185-2195(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22426065; PubMed=12537568;			
RA	Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,			
RA	Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,			
RA	George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,			
RA	Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,			
RA	Swaiskac R., Taber P.E., Wan K., Stepleton M., Sutton G.G., Venter C.,			
RA	Weinstock R., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,			
RT	"Finishing a whole-genome shotgun: Release 3 of the <i>Drosophila</i>			
RT	melanogaster whole-genome genome sequence.";			
RL	Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22426070; PubMed=12537573;			
RA	Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,			
RA	Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,			
RA	Ashburner M., Celniker S.E.;			
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin:"			

RT	a	genomics perspective."
RL	Genome Biol.	3:RESEARCH0084-RESEARCH0084(2002).
RN	[4]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22426069;	PubMed=12537572;
RA	Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	
RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	
RA	Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Bernan B.P.,	
RA	Bettencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,	
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,	
RA	Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	
RA	Lewis S.E.;	
RT	"Annotation of the Drosophila melanogaster euchromatic genome: a	
RT	systematic review."	
RL	Genome Biol.	3:RESEARCH0083-RESEARCH0083(2002).
RN	[5]	
RP	SEQUENCE FROM N.A.	
RG	FlyBase:	
RL	Submitted (SEP-2002)	to the EMBL/GenBank/DDBJ databases.
RN	[6]	
RP	SEQUENCE FROM N.A.	
RG	FlyBase:	
RL	Submitted (MAR-2004)	to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF003700; AAFC4943.1;	--
DR	InFAct; Q9YEV6;	--
SQ	FlyBase; FBgn0040553; CG14374.	
Query Match	Best Local Similarity	60.5%; Score 46; DB 2; Length 99;
Matches	9; Conservative	0; Mismatches 5; Indels 0; Gaps 0.
OY	2	APKYEAYKAAPA 15
Ddb	47	APAYSTYAAAVPA 60
RESULT 5		
O6YST4		
ID	O6YST4	PRELIMINARY; PRT; 299 AA.
AC	O6YST4	
DT	05-JUL-2004	(TREMBLrel. 27, Created)
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)
DE	05-JUL-2004	(TREMBLrel. 27, Last annotation update)
GN	Hypotheical protein P0680C01.22.	
OS	Oryza sativa (japonica cultivar-group).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC	Ehharctoidae; Oryzaceae; Oryza.	
OX	NCBI_TaxID=39947;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Sasaki T., Matsumoto T., Katayose Y.;	
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC	
RT	clone:P0680C01."	
RL	Submitted (APR-2003)	to the EMBL/GenBank/DDBJ databaes.
DR	EMBL; AP006344; BA084796.1;	--
KM	Hypotheical protein.	
SQ	SEQUENCE	299 AA; 31850 MW; 4C14C4070BC31552 CRC64;
Query Match	Best Local Similarity	59.2%; Score 45; DB 2; Length 299;
Matches	11; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	1	EAPKYEAYKAAPA 15
Ddb	262	EAPKYEATPAAATA 276
RESULT 6		
ID	Q7S7R7	PRELIMINARY; PRT; 408 AA.

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AC 075787;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Probable translation elongation factor eEF-1,
  gamma chain).
GN Name=NCU03826.1; Synonyms=82C3.020;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
  Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Renman B.,
  Elkins I., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
  Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M.,
  Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
  Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
  Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
  Kamal M., Kamyszelis M., Mauceli E., Bielke C., Rude S., Frisman D.,
  Kysiofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
  Cogoni C., Macho G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
  Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
  Yarden O., Plamann M., Sells S., Dunlap J., Radford A., Aramayo R.,
  Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Preilag M.,
  Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,
  RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
  RT Nature 0:0-(2003).
  RN [2]
  RP SEQUENCE FROM N.A.
  RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
  RA Nyakatura G., Mewes H.W., Manhaupt G.;
  RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
  RN [3]
  RP SEQUENCE FROM N.A.
  RA German Neurospora genome project;
  RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
  CC -1- CAUTION: The sequence shown here is derived from an
  CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  CC Preliminary data.
  CC
  DR EMBL; AABX0100273; EAA31979.1; -.
  DR EMBL; BX842617; CAE76104.1; -.
  DR HSSP; P29547; INHY.
  DR GO; GO:0005853; Cytokaryotic translation elongation factor 1 . . .; IEA.
  DR GO; GO:0003746; P:translation elongation factor activity; IEA.
  DR GO; GO:0006144; P:translational elongation; IEA.
  DR InterPro; IPR001662; EFL_G.
  DR InterPro; IPR004046; GST_Cterm.
  DR InterPro; IPR010987; GST_C like.
  DR InterPro; IPR004045; GST_Nterm.
  DR Pfam; PF00647; EFLG; 1.
  DR Pfam; PF00063; GST_C; 1.
  DR Pfam; PF02788; GST_N; 1.
  DR ProDom; PD006217; EFL_G; 1.
  DR ProSITE; PS50040; EFLG; 1.
  KM Elongation factor; Hypothetical protein.
  SQ SEQUENCE 408 AA; 45741 MW; D5ABC7A3D1D6B178 CRC64;
  Query Match 59.2%; Score 45; DB 2; Length 408;
  Best Local Similarity 73.3%; Pred. No. 43;
  Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 1 EAPKYEAYKAAPA 15
  Db 222 EAPKPAAPKPAAPA 236
  RESULT 7
  MLEF MOUSE STANDARD; PRT; 192 AA.
  AC P09541;

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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myosin light chain 1, atrial/fetal isoform (MLC1A) (MTC1EMB).
GN Name=MLC1a; Synonyms=My1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=88315068; PubMed=2842339;
RA Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,
  RA Buckingham M.E.;
  RT "Structure and sequence of the myosin alkali light chain gene
  RT expressed in adult cardiac atria and fetal striated muscle.";
  RL J. Biol. Chem. 263:12669-12676(1988).
  RN [2]
  RP SEQUENCE OF 1-40 FROM N.A.
  RC STRAIN=C3H;
  RX MEDLINE=89057447; PubMed=3194193;
  RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
  RA Buckingham M.E.;
  RT "Promoter analysis of myosin alkali light chain genes expressed in
  RT muscle striated muscle.";
  RL Nucleic Acids Res. 16:10037-10052(1988).
  CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
  CC chains.
  CC -1- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal
  CC skeletal and ventricular muscle.
  CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
  CC PROTEIN DOES NOT BIND CALCIUM.
  CC
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  CC or send an email to license@isb-sib.ch).
  CC
  DR EMBL; M20772; AAA39721.1; -.
  DR EMBL; M31017; AAA39721.1; JOINED.
  DR EMBL; M20769; AAA39721.1; JOINED.
  DR EMBL; M20770; AAA39721.1; JOINED.
  DR EMBL; M20771; AAA39721.1; JOINED.
  DR EMBL; X12971; AAA31414.1; -.
  DR EMBL; M19436; AAA39720.1; -.
  DR PIR; A31114; MCM5AE.
  DR HSSP; P02607; 1BR1.
  DR MCD; MGI:97267; My1a.
  DR InterPro; IPR002048; EF-hand.
  DR InterPro; IPR010983; EF_Hand like.
  DR ProDom; PD000012; EF-hand; 2.
  KM Multigene family; Muscle protein; Myosin.
  FT INIT MET 0
  SQ SEQUENCE 192 AA; 21028 MW; B0439D512FA19C38 CRC64;
  Query Match 57.9%; Score 44; DB 1; Length 192;
  Best Local Similarity 76.9%; Pred. No. 30;
  Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 3 PKYEAYKAAPA 15
  Db 7 PKKEAPKPAAPA 19
  RESULT 8
  O6C9V2 PRELIMINARY; PRT; 316 AA.
  AC O6C9V2;
  DT 25-OCT-2004 (TrEMBLrel. 28, Created)

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DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DE 25-OCT-2004 (TReMBLrel. 28, last annotation update)
 DE Similar to gp|P36110 Saccharomyces cerevisiae YKR013w PRY2
 protein.
 GN ORFNames=YAL10D08140g;
 OS Yarrowia lipolytica CL1899.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 ON NCBI_TaxID=284591;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1899;
 RG Genolenvures;
 RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Dujon B., Sheehan D., de Montigny J., Marc C., Neuveglise C., Talla E.,
 RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barde V.,
 RA Barnay S., Bianchin S., Beckerich J.M., Beyne E., Blyksten C.,
 RA Bolstrame A., Boyer J., Cattoi L., Confiantieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Smeunne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1899;
 RA Genoscope; (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; CR382130; CAG80748.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR001283; Allrgn_V5/Tp1.
 DR Pfam; PF00188; SCP.1
 DR PRINTS; PRD0837; V5TPX1KE.
 DR ProDom; PD000542; Allrgn_V5/Tp1; 1.
 DR SMART; SM00198; SCP.1.
 DR POSITE; PS01009; CRISP.1; 1.
 SQ SEQUENCE 316 AA; 33458 MW; F88EDA9F938631B5 CRC64;
 Query Match 57.9%; Score 44; DB 2; Length 316;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EAPRYEAYKAAAPA 15
 Db 126 EAPKQKAPKSEAPS 140
 |||||
 RESULT 9
 Q73BN9 PRELIMINARY; PRT; 424 AA.
 AC Q73BN9;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
 DE 2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide
 DE succinyltransferase (EC 2.3.1.61)
 GN Name=cdhB; OrderedLocNames=BCE1379;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacillia; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=222523;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shroto K.A., Fouts D.E., Tourasse N.J., Anguilo S.V., Kolonay J.F.,
 RA Nelson W.C., Kojstoe A.-B., Fraser C.M., Read T.D.,
 "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic

RT adaptations and a large plasmid related to Bacillus anthracis pX01."
 RL Nucleic Acids Res. 32:977-988(2004).
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
 DR EMBL; AE017268; AAS40308.1; -;
 DR HSSP; P11961; 1B55.
 DR TIGR; BCE1379; -;
 DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransferase; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro; IPR001078; 2-oxoacid dh.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR011053; Hybrid_motif.
 DR InterPro; IPR003016; Lipoyl_BS.
 DR InterPro; IPR006255; SUCB.
 DR InterPro; IPR010915; TONB_Box_N.
 DR Pfam; PF00198; 2-oxoacid dh; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR ProDom; PD001115; 2-oxoacid dh; 1.
 DR TIGRFAMs; TIGR01347; SUCB; 1.
 DR PROSITE; PS00189; LIPOYL; 1.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 KM Acyltransferase; Complete proteome; Lipoyl; Transferase.
 SQ SEQUENCE 424 AA; 45794 MW; B61F0CF90B7BA54C CRC64;
 Query Match 57.9%; Score 44; DB 2; Length 424;
 Best Local Similarity 73.3%; Pred. No. 66;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EAPRYEAYKAAAPA 15
 Db 100 EAPKQKAPKSEAPS 114
 |||||
 RESULT 10
 Q869Y7 PRELIMINARY; PRT; 439 AA.
 AC Q869Y7;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE Similar to Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 DE dihydrolipoamide succinyltransferase component of 2-oxoglutarate
 DE dehydrogenase complex, mitochondrial (EC 2.3.1.61) (E2) (E2K).
 OS Dicyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 ON NCBI_TaxID=44689;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Eichinger L., Szafrański K., Pacheco J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Galgo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
 DR EMBL; AC116305; AAO52267.1; -;
 DR HSSP; P07016; 1C4T.
 DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransferase; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.

DR ProDom; PD000139; FAD_pyr_redox; 1

DR	EMBL: AY133249: AAN28309.1: -
KL	func. integr. genome v: v-v (2002)

DR	EMBL: AY133249: AAN28309.1: -
KL	func. integr. genome v:v-v (2002/

SEQ SEQUENCE '802 AA; 87457 MW; 6D08FC195164B46F CRC64;

Query Match 57.9%; Score 44; DB 2; Length 802;

Best Local Similarity 66.7%; Pred. No. 1.2e+02; Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPRYEAYKAAAPAA 15
| | | | |
DQ 246 EAPKPKLASAPAPAA 260

RESULT 14

RS3_STRCO STANDARD; PRT; 277 AA.

AC 09L0D4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S3.
GN Name=rpSC; OrderedLocustNames=SC04708; ORFNames=SCD31.33;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145.
RX MBLINB=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Honeyby T., Howarth S.,
RA Hwang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajadream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Snaap S., Squares R., Taylor K.,
RA Warren T., Metcortek A., Woodward J.R., Barrell J.B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)";
RL Nature 417:141-147(2002).
CC -1- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
in the 70S ribosome, positioning it for translation (By
similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
with proteins S10 and S14 (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein S3P family.
CC -1- SIMILARITY: Contains 1 KH type-2 domain.
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CC -----
DR EMBL, AL393121, CAB82076.1; -
DR HAVAP; MF_01309; -; 1.
DR InterPro; IPR004087; KH.
DR InterPro; IPR009019; KH prok.
DR InterPro; IPR004044; KH type-2.
DR InterPro; IPR001351; Ribosomal_S3_C.
DR InterPro; IPR008282; Ribosomal_S3_N.
DR InterPro; IPR005704; S3_bact.
DR Pfam; PF00013; KH; 1.
DR Pfam; PF00189; Ribosomal_S3_C; 1.
DR Pfam; PF00417; Ribosomal_S3_N; 1.
DR SMART; SM00332; KH; 1.
DR TIGRfams; TIGR01009; rpSC_bact; 1.
DR PROSITE; PS50823; KH_type_2; 1.
DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
KM Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
FT DOMAIN 38 106 KH type-2.

SEQ SEQUENCE 277 AA; 30273 MW; 5831536B64018135 CRC64;

Query Match 57.2%; Score 43.5; DB 1; Length 277;

Best Local Similarity 80.0%; Pred. No. 53; Matches 12; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 EAPRYEAYKAAAPAA 15
| | | | |
DQ 257 EAPKAEK-PAAAPAA 270

RESULT 15

06JRS4 PRELIMINARY; PRT; 163 AA.

AC 06JRS4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Voltage-gated sodium channel cardiac isoform Nav1.5 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Guionaud C.T., Althaus H., Beegle A., Lis J.L., Mevissen M.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY321582; AAC83897.1; -
DR GO; GO:0005216; F:ion channel activity; IEA.
DR InterPro; IPR010526; Na trans assoc.
DR Pfam; PF06512; Na_trans_assoc; 1.
KM Ion channel.
FT NON_TER 1 1
FT NON_TER 163 163
SQ SEQUENCE 163 AA; 17448 MW; 1C58F8C0F2A13D0 CRC64;

Query Match 56.6%; Score 43; DB 2; Length 163;

Best Local Similarity 60.0%; Pred. No. 38; Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPRYEAYKAAAPAA 15
| | | | |
DQ 118 ETTSSREAYKAAAPAA 132

Search completed: February 26, 2005, 23:55:39
Job time : 67.2041 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 76.6837 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583A-65

Perfect score: 71

Sequence: 1 EKAKYENYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19908:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	15	5	ABP52271 HLA-DR2 m
2	71	100.0	15	5	ABP52298 HLA-DR2 m
3	71	100.0	17	5	ABP52294 HLA-DR2 m
4	71	100.0	17	5	ABP52296 HLA-DR2 m
5	71	100.0	19	5	ABP52295 HLA-DR2 m
6	65	91.5	15	5	ABP52270 HLA-DR2 m
7	63	88.7	15	5	ABP52301 HLA-DR2 m
8	62	87.3	17	5	ABP52303 HLA-DR2 m
9	61	85.9	15	5	ABP52291 HLA-DR2 m
10	61	85.9	15	5	ABP52263 HLA-DR2 m
11	60	84.5	15	5	ABP52272 HLA-DR2 m
12	59	83.1	15	5	ABP52259 HLA-DR2 m
13	59	83.1	15	5	ABP52257 HLA-DR2 m
14	58	81.7	17	5	ABP52302 HLA-DR2 m
15	57	80.3	15	5	ABP52297 HLA-DR2 m
16	56	78.9	15	5	ABP52253 HLA-DR2 m
17	56	78.9	15	5	ABP52251 HLA-DR2 m
18	56	78.9	15	5	ABP52239 HLA-DR2 m
19	55	77.5	15	5	ABP52290 HLA-DR2 m
20	55	77.5	15	5	ABP52261 HLA-DR2 m
21	55	77.5	15	5	ABP52244 HLA-DR2 m
22	55	77.5	15	5	ABP52292 HLA-DR2 m
23	55	77.5	15	5	ABP52269 HLA-DR2 m
24	55	77.5	15	5	ABP52262 HLA-DR2 m
25	54	76.1	15	5	ABP52264 HLA-DR2 m

26	54	76.1	15	5	ABP52267 HLA-DR2 m
27	54	76.1	15	5	ABP52236 HLA-DR2 m
28	53	74.6	15	5	ABP52299 HLA-DR2 m
29	52	73.2	15	5	ABP52265 HLA-DR2 m
30	51	71.8	15	5	ABP52254 HLA-DR2 m
31	51	71.8	15	5	ABP52255 HLA-DR2 m
32	51	71.8	15	5	ABP52240 HLA-DR2 m
33	51	71.8	15	5	ABP52241 HLA-DR2 m
34	51	71.8	15	5	ABP52304 HLA-DR2 m
35	51	71.8	15	5	ABP52248 HLA-DR2 m
36	51	71.8	15	5	ABP52249 HLA-DR2 m
37	50	70.4	15	5	ABP52232 HLA-DR2 m
38	50	70.4	15	5	ABP52268 HLA-DR2 m
39	50	70.4	15	5	ABP52231 HLA-DR2 m
40	49	69.0	15	5	ABP52235 HLA-DR2 m
41	49	69.0	15	5	ABP52250 HLA-DR2 m
42	48	67.6	15	5	ABP52277 HLA-DR2 m
43	48	67.6	15	5	ABP52238 HLA-DR2 m
44	48	67.6	15	5	ABP52243 HLA-DR2 m
45	48	67.6	15	5	ABP52280 HLA-DR2 m

ALIGNMENTS

RESULT 1	ABP52271	standard; peptide; 15 AA.
ID	ABP52271	
XX	ABP52271;	
AC	16-OCT-2002 (first entry)	
DT	16-OCT-2002 (first entry)	
XX	HLA-DR2 molecule binding peptide SEQ ID NO:65.	
DE	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;	
XX	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;	
KW	immune response; antiinflammatory; neuroprotective; proliferation;	
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;	
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;	
KW	anti-tumour necrosis factor agent.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	WO200259143-A2.	
PN	01-AUG-2002.	
XX	24-JAN-2002; 2002MO-US002071.	
PF	24-JAN-2001; 2001US-0263569P.	
XX	(HARD) HARVARD COLLEGE.	
PA	Strominger JL, Fridkis-Hareli M;	
XX	WPI; 2002-608439/65.	
PI	New compositions comprising synthetic peptides in complex with a major	
PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a	
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral	
PT	encephalomyelitis.	
XX	Claim 28; Page 39; 54pp; English.	
PS	The present invention describes compositions (I) comprising a peptide	
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine	
CC	residues. The complex of the peptide with a major histocompatibility	
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an	
CC	immune response. (I) has antiinflammatory and neuroprotective activities,	
CC	and can be used as a MHC class II protein inhibitor. The compositions	
CC	comprising the peptides are useful for treating demyelinating diseases	

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
1 EKAKYEAYKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
RESULT 2
ID ABP52298 standard; peptide; 15 AA.
XX
AC ABP52298;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
XX
KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 15 AA;
Query Match 100.0%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
1 EKAKYEAYKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
RESULT 3
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 71; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15

Db 3 EKAKYEAYKAAAAA 17

RESULT 4
ID ABP52296 standard; peptide; 17 AA.

AC ABP52296;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:90.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

SQ Sequence 17 AA;

Query Match 100.0%; Score 71; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 1 EKAKYEAYKAAAAA 15

RESULT 5
ID ABP52295 standard; peptide; 19 AA.

XX ABP52295;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:89.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

SQ Sequence 19 AA;

Query Match 100.0%; Score 71; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 3 EKAKYEAYKAAAAA 17

RESULT 6
ID ABP52270 standard; peptide; 15 AA.

AC ABP52270;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:64.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.
 PF 24-JAN-2002; 2002WO-US002071.
 PR 24-JAN-2001; 2001US-0263569P.
 XX (HARD) HARVARD COLLEGE.
 PA Strominger JL, Fridkis-Hareli M,
 PI WPI; 2002-608439/65.
 PS Claim 28; Page 39; 54pp; English.
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 CC XX
 SQ Sequence 15 AA;
 Query Match 91.5%; Score 65; DB 5; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.00054;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EKAKEAYKRAAAAA 15
 DB 1 EAKKEAYKRAAAAA 15
 RESULT 7
 ID ABP52301 standard; peptide; 15 AA.
 AC ABP52301;
 XX 16-OCT-2002 (first entry)
 DE HLA-DR2 molecule binding peptide SEQ ID NO:95.
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.
 PF 24-JAN-2002; 2002WO-US002071.
 PR 24-JAN-2001; 2001US-0263569P.
 XX (HARD) HARVARD COLLEGE.
 PA Strominger JL, Fridkis-Hareli M,
 PI WPI; 2002-608439/65.
 PS Claim 28; Page 39; 54pp; English.
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 CC XX
 SQ Sequence 15 AA;
 Query Match 88.7%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0012;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKAKEAYKRAAAAA 15
 DB 1 EAKKEAYKRAAAAA 15
 RESULT 8
 ID ABP52303 standard; peptide; 17 AA.
 AC ABP52303;
 XX 16-OCT-2002 (first entry)
 DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.

OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.
 PF 24-JAN-2002; 2002WO-US002071.
 PR 24-JAN-2001; 2001US-0263569P.
 XX (HARD) HARVARD COLLEGE.
 PA Strominger JL, Fridkis-Hareli M,
 PI WPI; 2002-608439/65.
 PS Claim 28; Page 39; 54pp; English.
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 CC XX
 SQ Sequence 15 AA;
 Query Match 88.7%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0012;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKAKEAYKRAAAAA 15
 DB 1 EAKKEAYKRAAAAA 15
 RESULT 8
 ID ABP52303 standard; peptide; 17 AA.
 AC ABP52303;
 XX 16-OCT-2002 (first entry)
 DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 17 AA;

Query Match 87.3%; Score 62; DB 5; Length 17;
 Best Local Similarity 86.7%; Pred. No. 0.0019;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15
 |||:|||||||
 Db 3 EKAKFEAYKAAAAA 17

RESULT 9
 ABP52291
 ID ABP52291 standard; peptide; 15 AA.
 XX
 AC ABP52291;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;

XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 15 AA;

Query Match 85.9%; Score 61; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0025;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15
 |||:|||||||
 Db 1 EKAKFEAYKAAAAA 15

RESULT 10
 ABP52263
 ID ABP52263 standard; peptide; 15 AA.
 XX
 AC ABP52263;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:57.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX Example 1; Page 33; 54pp; English.

PS The present invention describes compositions (I) comprising a peptide

XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

SQ

Query Match 85.9%; Score 61; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0025;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAKYEAAYKAAAAA 15

DB 1 EAKYEAAYKAAAAA 15

RESULT 11

ABP52272

ID ABP52272 standard; peptide; 15 AA.

XX

AC ABP52272;

XX

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:66.

XX

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KM immune response; antiinflammatory; neuroprotective; proliferation;

KM MHC class II protein inhibitor; demyelinating disease; inhibition;

KM post-viral encephalomyelitis; post-vaccine demyelinating condition;

KM anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

XX WPI; 2002-608439/65.

XX

PT New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

SQ

Query Match 84.5%; Score 60; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0036;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAKYEAAYKAAAAA 15

DB 1 EAKYEAAYKAAAAA 15

RESULT 12

ABP52259

ID ABP52259 standard; peptide; 15 AA.

XX

AC ABP52259;

XX

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:53.

XX

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KM immune response; antiinflammatory; neuroprotective; proliferation;

KM MHC class II protein inhibitor; demyelinating disease; inhibition;

KM post-viral encephalomyelitis; post-vaccine demyelinating condition;

KM anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

XX WPI; 2002-608439/65.

XX

PT New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Example 1; Page 33; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

Query Match	83.1%;	Score 59;	DB 5;	Length 15;
Best Local Similarity	86.7%;	Pred. No. 0.0053;		

Db 3 EKAKEFAFKAAAAPA 17

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RESULT 15
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 5app; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

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Query Match 80.3%; Score 57; DB 5; Length 15;
 Best Local Similarity 80.0%; Pred. No. 0.011;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EKAKYENAKAAAAA 15
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Db 1 EKPKFAYKAAAPA 15

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Search completed: February 26, 2005, 23:48:21
 Job time : 79.6837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 20.051 Seconds
(without alignments)
55.844 Million cell updates/sec

Title: US-10-056-583A-65
Perfect score: 71
Sequence: 1 EKAKYKAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	59.2	13	5	PCT-US95-04121-38
2	42	59.2	1001	4	US-09-248-796A-18658
3	41	57.7	402	4	US-09-248-796A-17859
4	40	56.3	13	5	PCT-US94-10257A-33
5	40	56.3	109	4	US-09-405-743A-7
6	40	56.3	109	4	US-09-816-989A-7
7	40	56.3	466	4	US-09-489-039A-13950
8	40	56.3	1156	4	US-09-198-452A-171
9	40	56.3	1562	4	US-09-438-185A-152
10	39	54.9	497	1	US-08-295-670-6
11	39	54.9	497	1	US-08-633-485-6
12	39	54.9	510	3	US-08-508-761B-4
13	39	54.9	601	4	US-09-252-991A-21824
14	39	54.9	731	4	US-09-252-991A-18769
15	38	53.5	186	4	US-09-902-540-11242
16	38	53.5	576	4	US-09-543-681A-7747
17	38	53.5	582	4	US-09-918-497-100
18	38	53.5	759	4	US-09-328-352-4241
19	37.5	52.8	391	4	US-09-902-540-11110
20	37	52.1	38	3	US-09-117-121-16
21	37	52.1	38	4	US-09-117-121-24
22	37	52.1	38	4	US-09-344-529-5
23	37	52.1	56	4	US-09-405-743A-3
24	37	52.1	56	4	US-09-816-989A-3
25	37	52.1	77	4	US-09-405-743A-5
26	37	52.1	77	4	US-09-816-989A-5
27	37	52.1	86	4	US-09-405-743A-6

28	37	52.1	86	4	US-09-816-989A-6	Sequence 6, Appli
29	37	52.1	143	4	US-09-270-767-33766	Sequence 33766, A
30	37	52.1	143	4	US-09-270-767-48983	Sequence 48983, A
31	37	52.1	459	4	US-09-543-681A-5116	Sequence 5116, Ap
32	37	52.1	596	2	US-08-836-620A-16	Sequence 16, Appl
33	37	52.1	615	4	US-09-902-540-10642	Sequence 10642, A
34	37	52.1	802	3	US-09-489-039A-11230	Sequence 11230, A
35	37	52.1	958	1	US-08-426-236-4	Sequence 4, Appli
36	36.5	51.4	45	4	US-09-405-743A-2	Sequence 2, Appli
37	36.5	51.4	45	4	US-09-816-989A-2	Sequence 2, Appli
38	36	50.7	13	5	PCT-US95-04121-60	Sequence 60, Appl
39	36	50.7	54	3	US-09-117-121-30	Sequence 30, Appl
40	36	50.7	166	4	US-09-252-991A-22139	Sequence 22139, A
41	36	50.7	180	6	5273901-7	Patent No. 5273901
42	36	50.7	180	6	5482709-6	Patent No. 5482709
43	36	50.7	180	6	5273901-7	Patent No. 5273901
44	36	50.7	180	6	5482709-6	Patent No. 5482709
45	36	50.7	209	4	US-09-489-039A-12638	Sequence 12638, A

ALIGNMENTS

RESULT 1
PCT-US95-04121-38
Sequence 38, Application PC/TUS9504121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-04121-38
Query Match 59.2% Score 42; DB 5; Length 13;
Best Local Similarity 76.9% Pred. No. 0.92;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 3 AKTEAYKAAAAA 15
1 AAYKAAKAAAAA 13
RESULT 2
US-09-248-796A-18658
Sequence 18658, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18658
LENGTH: 1001
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (21)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-248-796A-18658

Query Match 59.2%; Score 42; DB 4; Length 1001;
Best Local Similarity 78.6%; Pred. No. 78;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 KAKYEAAYKAAA 15
DB 818 KAKEBAAYKAAA 831

RESULT 3
US-09-248-796A-17859
Sequence 17859, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17859
LENGTH: 402
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17859

Query Match 57.7%; Score 41; DB 4; Length 402;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KAKYEAAYKAA 11
DB 70 KAKYESYDAA 79

RESULT 4
PCT-US94-10257A-33
Sequence 33, Application PC/TUS9410257A
GENERAL INFORMATION:
APPLICANT: IMMUTOLOGIC PHARMACEUTICAL CORPORATION
APPLICANT: BRIGITTE DEVUOX
APPLICANT: JONATHAN B. ROTHBARD
APPLICANT: DAWN SMILEK
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUTOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10257A
FILING DATE: 1 SEPTEMBER 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,824
FILING DATE: 03-SEP-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANNE I CRAIG
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 071.1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-10257A-33

Query Match 56.3%; Score 40; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 AKYEAAYKAAA 15
DB 1 AAYAAKAAAAA 13

RESULT 5
US-09-405-743A-7
Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-7

Query Match 56.3%; Score 40; DB 4; Length 109;
Best Local Similarity 81.8%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KAKYEAAYKAA 12
DB 55 KAKEAYKAA 65

RESULT 6
US-09-816-989A-7
; Sequence 7, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lie, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-7

Query Match 56.3%; Score 40; DB 4; Length 109;
Best Local Similarity 81.8%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAKYAYKAA 12
DB 55 KAKYAYKAA 65

RESULT 7
US-09-489-039A-13950
; Sequence 13950, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709/2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13950
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950

Query Match 56.3%; Score 40; DB 4; Length 466;
Best Local Similarity 76.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYAYKAA 15
DB 153 ASLEAYKAA 165

RESULT 8
US-09-198-452A-171
; Sequence 171, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 171
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-171

Query Match 56.3%; Score 40; DB 4; Length 1156;
Best Local Similarity 64.3%; Pred. No. 1,9e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAYEYKAA 14
DB 659 EKSYDNEKAA 672

RESULT 9
US-09-438-185A-152
; Sequence 152, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 1562
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0150
US-09-438-185A-152

Query Match 56.3%; Score 40; DB 4; Length 1562;
Best Local Similarity 64.3%; Pred. No. 2.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAYEYKAA 14
DB 1065 EKSYDNEKAA 1078

RESULT 10
US-08-295-670-6
; Sequence 6, Application US/08295670
; Patent No. 5547864
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: MIWA, KIYOSHI
; APPLICANT: KAWAHARA, YOSHIO
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,670
FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-4069
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5547664man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-697-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-295-670-6

Query Match 54.9%; Score 39; DB 1; Length 497;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKEAYKRAAAAA 15
DB 104 EQAAVEAFEAARVA 118

RESULT 11
US-08-633-485-6
Sequence 6, Application US/08633485
Patent No. 5681717
GENERAL INFORMATION:
APPLICANT: KAWASAKI, HISASHI
APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MIWA, KIYOSHI
APPLICANT: KAWAHARA, YOSHIO
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,485
FILING DATE: 17-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/295,670

FILING DATE: 08-SEP-1994
APPLICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-4069
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5681717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-697-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-633-485-6

Query Match 54.9%; Score 39; DB 1; Length 497;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKEAYKRAAAAA 15
DB 104 EQAAVEAFEAARVA 118

RESULT 12
US-08-508-761B-4
Sequence 4, Application US/08508761B
Patent No. 6027920
GENERAL INFORMATION:
APPLICANT: Joliff, Gwennael
APPLICANT: Guyonvarch, Arnel
APPLICANT: Duchiton, Francis
APPLICANT: Renaud, Michel
TITLE OF INVENTION: System for Protein Expression and
TITLE OF INVENTION: Secretion Especially in Corynebacteria
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,761B
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

Query Match 54.9%; Score 39; DB 4; Length 731;

Search completed: February 26, 2005, 23:59:27
Job time : 22.051 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 : Search time 53.5714 Seconds
(without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583a-65
Perfect score: 71
Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	15	US-10-056-583-65	Sequence 65, Appl
2	71	100.0	17	US-10-056-583-88	Sequence 88, Appl
3	71	100.0	17	US-10-056-583-90	Sequence 90, Appl
4	71	100.0	19	US-10-056-583-89	Sequence 89, Appl
5	65	91.5	15	US-10-056-583-64	Sequence 64, Appl
6	63	88.7	15	US-10-056-583-95	Sequence 95, Appl
7	62	87.3	15	US-10-056-583-92	Sequence 92, Appl
8	62	87.3	17	US-10-056-583-97	Sequence 97, Appl
9	61	85.9	15	US-10-056-583-57	Sequence 57, Appl
10	61	85.9	15	US-10-056-583-85	Sequence 85, Appl
11	59	83.1	15	US-10-056-583-66	Sequence 66, Appl
12	59	83.1	15	US-10-056-583-51	Sequence 51, Appl
13	59	83.1	15	US-10-056-583-53	Sequence 53, Appl

14	58	81.7	17	US-10-056-583-96	Sequence 96, Appl
15	57	80.3	15	US-10-056-583-91	Sequence 91, Appl
16	56	78.9	15	US-10-056-583-33	Sequence 33, Appl
17	56	78.9	15	US-10-056-583-45	Sequence 45, Appl
18	56	78.9	15	US-10-056-583-47	Sequence 47, Appl
19	55	77.5	15	US-10-056-583-38	Sequence 38, Appl
20	55	77.5	15	US-10-056-583-55	Sequence 55, Appl
21	55	77.5	15	US-10-056-583-56	Sequence 56, Appl
22	55	77.5	15	US-10-056-583-63	Sequence 63, Appl
23	55	77.5	15	US-10-056-583-84	Sequence 84, Appl
24	55	77.5	15	US-10-056-583-86	Sequence 86, Appl
25	54	76.1	15	US-10-056-583-30	Sequence 30, Appl
26	54	76.1	15	US-10-056-583-58	Sequence 58, Appl
27	54	76.1	15	US-10-056-583-61	Sequence 61, Appl
28	53	74.6	15	US-10-056-583-93	Sequence 93, Appl
29	52	73.2	15	US-10-056-583-99	Sequence 99, Appl
30	51	71.8	15	US-10-056-583-34	Sequence 34, Appl
31	51	71.8	15	US-10-056-583-35	Sequence 35, Appl
32	51	71.8	15	US-10-056-583-42	Sequence 42, Appl
33	51	71.8	15	US-10-056-583-43	Sequence 43, Appl
34	51	71.8	15	US-10-056-583-48	Sequence 48, Appl
35	51	71.8	15	US-10-056-583-49	Sequence 49, Appl
36	51	71.8	15	US-10-056-583-98	Sequence 98, Appl
37	50	70.4	15	US-10-056-583-25	Sequence 25, Appl
38	50	70.4	15	US-10-056-583-26	Sequence 26, Appl
39	50	70.4	15	US-10-056-583-62	Sequence 62, Appl
40	49	69.0	15	US-10-056-583-29	Sequence 29, Appl
41	49	69.0	15	US-10-056-583-44	Sequence 44, Appl
42	48	67.6	15	US-10-056-583-32	Sequence 32, Appl
43	48	67.6	15	US-10-056-583-37	Sequence 37, Appl
44	48	67.6	15	US-10-056-583-39	Sequence 39, Appl
45	48	67.6	15	US-10-056-583-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-65
Sequence 65, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridakis-Harell, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DENEUTINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 15
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match 100.0%; Score 71; DB 14; Length 15;
Best local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 1 EKAKYEAYKAAAAA 15

RESULT 2
US-10-056-583-88

```
/ Sequence 88, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 88
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

```
Query Match          100.0%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKAAAAA 15
        |||
        3 EKAKEYAYKAAAAA 17
```

```
RESULT 3
US-10-056-583-90
/ Sequence 90, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 90
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match          100.0%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKAAAAA 15
        |||
        1 EKAKEYAYKAAAAA 15
```

```
RESULT 4
US-10-056-583-89
/ Sequence 89, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
```

```
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 89
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match          100.0%; Score 71; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKAAAAA 15
        |||
        3 EKAKEYAYKAAAAA 17
```

```
RESULT 5
US-10-056-583-64
/ Sequence 64, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match          91.5%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00074;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKAAAAA 15
        |||
        1 EKAKEYAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-95
/ Sequence 95, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match      88.7%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. NO. 0.0015;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EKAKYEAAYKAAAAA 15
       |||:|||||
Db      1 EKAKFEAFKAAAAA 15

RESULT 7
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match      87.3%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. NO. 0.0022;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EKAKYEAAYKAAAAA 15
       |||:|||||
Db      1 EKAKYEAAYKAAAAA 15

RESULT 8
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; FEATURE:
```

```
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match      87.3%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. NO. 0.0025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EKAKYEAAYKAAAAA 15
       |||:|||||
Db      3 EKAKFEAFKAAAAA 17

RESULT 9
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match      85.9%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. NO. 0.0032;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EKAKYEAAYKAAAAA 15
       |||:|||||
Db      1 EKAKYEAAYKAAAAA 15

RESULT 10
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match 85.9%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0032;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKEYAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 1 EKPEYKAYKAAAAA 15

RESULT 11
US-10-056-583-66

Sequence 66, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 84.5%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0047;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKEYAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 1 EAKKEYAYKAAAAA 15

RESULT 12
US-10-056-583-51

Sequence 51, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Query Match 83.1%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0067;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKEYAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 1 EAKKAYAYKAAAAA 15

RESULT 13
US-10-056-583-53

Sequence 53, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53

Query Match 83.1%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0067;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKEYAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 1 EKAAYAYKAAAAA 15

RESULT 14
US-10-056-583-96

Sequence 96, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 96
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match 81.7%; Score 58; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKAKEYAYKAAAAA 15
| | | | | | | | | | | | | | | | |
Db 3 EKAKEAFKAAAAA 17

RESULT 15
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridakis-Harell, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match 80.3%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.014;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
| | : | | | | | | | | | | | | |
Db 1 EKPKFEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:22
Job time : 54.5714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 13.3163 Seconds
(without alignments)
108.382 Million cell updates/sec

Title: US-10-056-583A-65
Perfect score: 71
Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	60.6	185	2	S36290 T-cell receptor ga
2	42	59.2	179	2	F97683 50S ribosomal prot
3	42	59.2	179	2	AF2908 50S ribosomal prot
4	42	59.2	188	2	I50145 homeotic protein H
5	42	59.2	289	2	A43562 homeotic protein H
6	41.5	58.5	189	2	S77930 exoskeletal protei
7	41.5	58.5	189	2	S77935 exoskeletal protei
8	41	57.7	177	2	AD1367 peptidyl methionin
9	41	57.7	177	2	AD1679 peptidyl methionin
10	41	57.7	254	2	H86355 probable 14-3-3 pr
11	41	57.7	1885	1	JC4086 fatty-acid synthas
12	41	57.7	2129	2	T77431 hypothetical prote
13	40	56.3	73	2	S40015 phd protein - phag
14	40	56.3	377	2	T43037 probable fatty-aci
15	40	56.3	421	2	JV0057 tola protein - Esc
16	40	56.3	478	2	S04675 H+-transporting tw
17	40	56.3	806	2	T13690 hypothetical prote
18	40	56.3	1537	2	PE6509 Ctl147 hypothetical
19	40	56.3	1537	2	C81558 conserved hypotet
20	40	56.3	1537	2	H72112 ctl147 hypothetical
21	40	56.3	1842	2	T43409 probable fatty-aci
22	40	56.3	1842	2	T38781 fatty acid synthas
23	39	54.9	113	2	T30041 hypothetical prote
24	39	54.9	250	2	T51971 proteasome endopep
25	39	54.9	318	2	B48487 MCB (Tn339) - Ba
26	39	54.9	436	2	T31902 hypothetical prote
27	39	54.9	510	2	S35028 protein P82 precu
28	39	54.9	553	2	D83640 hypothetical prote
29	39	54.9	698	2	T32594 hypothetical prote

30	39	54.9	728	2	H82965 DNA helicase II PA
31	39	54.9	1430	2	T34516 hypothetical prote
32	39	54.9	2957	2	T33152 hypothetical prote
33	38	53.5	101	2	G75512 conserved hypotet
34	38	53.5	108	2	F97521 conserved hypotet
35	38	53.5	108	2	AH2740 conserved hypotet
36	38	53.5	140	2	D81970 H+-transporting tw
37	38	53.5	159	2	A97836 hypothetical prote
38	38	53.5	170	2	E81312 probable lipoprote
39	38	53.5	178	2	S03216 hypothetical prote
40	38	53.5	289	2	AC1399 hypothetical prote
41	38	53.5	346	2	C82156 conserved hypotet
42	38	53.5	368	2	B82357 conserved hypotet
43	38	53.5	398	2	T21061 hypothetical prote
44	38	53.5	433	2	D87408 ATPase, AAA family
45	38	53.5	478	2	E87470 efflux system prot

ALIGNMENTS

RESULT 1

S36290 T-cell receptor gamma chain precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36290; S23041
R:Hein, W.R.; Dudley, L.
EMBO J. 12, 715-724, 1993
A:Title: Divergent evolution of T cell repertoires: extensive diversity and development
A:Reference number: S36287; MUID:93178447; PMID:8440261
A:Accession: S36290
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-185 <HEI>
A:Cross-references: EMBL:Z12998; NID:G2260; PIDN:CAA78342.1; PID:G2261
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 60.6%; Score 43; DB 2; Length 185;
Best Local Similarity 66.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAA 12
DB 81 DKAKYVYKGA 92

RESULT 2

F97683 50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97683
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F97683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <KUR>
A:Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:G15157917; GSPDB: C:Genetics:
A:Gene: AGR C 4900
A:Map position: circular chromosome
C:Superfamily: Escherichia coli ribosomal protein L19
Query Match 59.2%; Score 42; DB 2; Length 179;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
|||:|||||
Db 137 EKARLEAEKVAQA 151

RESULT 3
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AF2908
R/Mod: D.W.; Serubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guentherer, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AF2908
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-179 <KUR>
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AL43684.1; PID:G17741210; GSPDB:C
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: rplS
A/Map position: circular chromosome
C/Superfamily: Escherichia coli ribosomal protein L19

Query Match 59.2%; Score 42; DB 2; Length 179;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
|||:|||||
Db 137 EKARLEAEKVAQA 151

RESULT 4
150145
homeotic protein Hox M - chicken
N/Alternate names: CHOX M
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C/Accession: 150145; S14512
R/Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A/Title: CDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viru
A/Reference number: 150145; MUID:91238215; PMID:1674560
A/Accession: 150145
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-188 <CRO>
A/Cross-references: UNIPROT:P23459; EMBL:X57158; NID:962700; PIDN:CAA40445.1; PID:962701
C/Genetics:
A/Gene: CHOX M
C/Superfamily: homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/96-152/Domain: homeobox homology <HOX>

Query Match 59.2%; Score 42; DB 2; Length 188;
Best Local Similarity 81.8%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
|:|||||
Db 10 YSKYKAAAAA 20

RESULT 5
A43562
homeotic protein Hox D8 - mouse

N/Alternate names: homeotic protein Hox 4.3
C/Species: Mus musculus (house mouse)
C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C/Accession: A43562
R/Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubo
Development 110, 733-745, 1990
A/Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob
A/Reference number: A43562; MUID:91209232; PMID:1982431
A/Accession: A43562
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-289 <IZP>
A/Cross-references: UNIPROT:P23463
C/Superfamily: homeotic protein Hox A7; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/196-252/Domain: homeobox homology <HOX>

Query Match 59.2%; Score 42; DB 2; Length 289;
Best Local Similarity 81.8%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
|:|||||
Db 10 YSKYKAAAAA 20

RESULT 6
S77930
exoskeletal protein HACP202A - American lobster (fragment)
C/Species: Homarus americanus (American lobster)
C/Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C/Accession: S77930
R/Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A/Description: Characterization of exoskeletal proteins from the American lobster, Homa
A/Reference number: S77925
A/Accession: S77930
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-189 <NOU>
A/Cross-references: UNIPROT:Q7M496

Query Match 58.5%; Score 41.5; DB 2; Length 189;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 EKAK-YEAYKAAAAA 15
|||:|||||
Db 11 EKARFPQAFKAAEAAA 26

RESULT 7
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C/Species: Homarus americanus (American lobster)
C/Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C/Accession: S77935
R/Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A/Description: Characterization of exoskeletal proteins from the American lobster, Homa
A/Reference number: S77925
A/Accession: S77935
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-189 <NOU>
A/Cross-references: UNIPROT:Q7M495

Query Match 58.5%; Score 41.5; DB 2; Length 189;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 EKAK-YEAYKAAAAA 15
|||:|||||

Db 11 EKARFQAFKAAEAAA 26

RESULT 8

AD1307

C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1307

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Karet, U.

Science 294, 849-852, 2001

A:Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maicournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1307

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-177 <GUA>

A:Cross-references: UNIPROT:Q8Y640; GB:NC_003210; PIDN:CAC9938.1; PID:G16411314; GSPDB:A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo1860

C:Superfamily: peptide methionine sulfoxide reductase

Query Match 57.7%; Score 41; DB 2; Length 177;
Best Local Similarity 53.3%; Pred. No. 14;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAAAA 15

Db 154 EKAYEGYQVAVSGRA 168

RESULT 9

AD1679

C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1679

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Karet, U.

Science 294, 849-852, 2001

A:Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maicournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-177 <GUA>

A:Cross-references: UNIPROT:Q92AE8; GB:AL592022; PIDN:CAC97204.1; PID:G16414475; GSPDB:A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lln1974

C:Superfamily: peptide methionine sulfoxide reductase

Query Match 57.7%; Score 41; DB 2; Length 177;
Best Local Similarity 53.3%; Pred. No. 14;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAAAA 15

Db 154 EKAYEGYQVAVSGRA 168

RESULT 10

H86355

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H86355

R:Ineologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.K.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: H86355

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-254 <STO>

A:Cross-references: UNIPROT:P48347; GB:AE05172; NID:G9392684; PIDN:AAE87261.1; GSPDB:A:Genetics:

A:Map position: 1

C:Superfamily: 14-3-3 protein

Query Match 57.7%; Score 41; DB 2; Length 254;
Best Local Similarity 90.0%; Pred. No. 20;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 EAYKAAAAA 15

Db 151 EAYKAAVAAA 160

RESULT 11

JC4086

C:Species: *Candida albicans*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: JC4086

R:Southard, S.B.; Chihlar, R.L.

Gene 156, 133-138, 1995

A:Title: Analysis and expression of the *Candida albicans* FAS2 gene.

A:Reference number: JC4086; MUID:9525657; PMID:7737507

A:Accession: JC4086

A:Molecule type: DNA

A:Residues: 1-1885 <STO>

A:Cross-references: UNIPROT:P43098; GB:I29063; NID:G456442; PIDN:AAA34345.1; PID:G45644

C:Genetics:

A:Gene: fas2

A:Map position: 3

C:Superfamily: yeast fatty-acid synthase

C:Keywords: acyltransferase; coenzyme A; fatty acid biosynthesis; phosphopantetheine; P

F;1299-1304/Region: cerulenin binding #status predicted

F;181/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 1885;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAKYEAAYKAA 11

Db 62 KAKYESYDAA 71

RESULT 12

T27431

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27431

R:Matthews, L.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20365

A:Accession: T27431

A:Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-2129 <ML>
 A/Cross-references: UNIPROT:Q9UIR8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP.Y
 A/Experimental source: clone Y79H2A
 C/Genetics:
 A/Gene: CESP:Y79H2A.3
 A/Intons: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67
 ; 1760/1; 1929/3; 2037/3; 2074/3

Query Match 57.7%; Score 41; DB 2; Length 2129;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKEAYKAA 12
 |||||
 Db 144 EYAKERYRMA 155

RESULT 13

S40015
 phd protein - phage P1
 C/Species: phage P1
 C/Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: S40015; S38553
 R/Lehner, H.; Maguin, E.; Jaffri, S.; Yarmolinsky, M.B.
 J. Mol. Biol. 233, 414-428, 1993
 A/Title: Plasmid addiction genes of bacteriophage P1: doc, which causes cell death on cu
 A/Reference number: S40015; MUID:94016561; PMID:8411153
 A/Accession: S40015
 A/Molecule type: DNA
 A/Residues: 1-73 <LEH>
 A/Cross-references: UNIPROT:Q06253; GB:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645
 R/Schmidt, C.; Lehner, H.; Guidolin, A.; Arber, W.
 Submitted to the EMBL Data Library, November 1992
 A/Description: Additional late promoter sequences of bacteriophage P1.
 A/Reference number: S38553
 A/Accession: S38553
 A/Molecule type: DNA
 A/Residues: 1-73 <SCH>
 A/Cross-references: EMBL:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

Query Match 56.3%; Score 40; DB 2; Length 73;
 Best Local Similarity 64.3%; Pred. No. 8.8;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KAKTEAYKAAAA 15
 |||||
 Db 41 KATFEAYKKAALDA 54

RESULT 14

T43037
 probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy
 C/Species: Schizosaccharomyces pombe
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43037
 R/Yoshioke, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997

A/Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A/Reference number: Z17323; MUID:98162722; PMID:9501991

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-377 <YOS>

A/Cross-references: UNIPROT:P78866; EMBL:DB9216; NID:g1749639; PIDN:BA13877.1; PID:g174
 A/Experimental source: strain PR745

C/Function:
 A/pathway: fatty acid biosynthesis

C/Superfamily: Yeast fatty-acid synthase
 C/Keywords: acyltransferase; coenzyme A; fatty acid biosynthesis

Query Match 56.3%; Score 40; DB 2; Length 377;
 Best Local Similarity 57.1%; Pred. No. 42;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKEAYKAAAA 14
 :|||
 Db 160 DEATYNAVYKAKTAA 173

RESULT 15

JV0057
 tola protein - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: JV0057; B64810
 R/Levengood, S.K.; Webster, R.E.
 J. Bacteriol. 171, 6600-6609, 1989
 A/Title: Nucleotide sequences of the tola and tolB genes and localization of their produ
 A/Reference number: JV0057; MUID:90078104; PMID:2687247
 A/Accession: JV0057

A/Molecule type: DNA
 A/Residues: 1-421 <LEV>

A/Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
 A/Experimental source: strain JM105

A/Note: the authors translated the initiation codon GTG for residue 1 as Val
 R/Battnay, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: B64810

A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA

A/Residues: 1-421 <BLAT>

A/Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AACT3833.1; PID:g1786960,
 A/Experimental source: strain K-12, substrain MG155

A/Comment: tola and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
 C/Genetics:

A/Map position: 17 min

A/Start codon: GTG
 C/Keywords: nucleotide binding; P-loop; transmembrane protein

F/14-34/Domain: transmembrane #status predicted <MSS>
 F/78-301/Domain: helical #status predicted <HSP>
 F/355-362/Region: nucleotide-binding motif A (P-loop)

Query Match 56.3%; Score 40; DB 2; Length 421;
 Best Local Similarity 76.9%; Pred. No. 47;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EKAKEAYKAAAA 13
 |||||
 Db 217 EKAKEAEKAAAA 229

Search completed: February 26, 2005, 23:57:12
 Job time : 17.3163 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 / Search time 65.2041 Seconds
(Without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583A-65

Perfect score: 71

Sequence: 1 EKAKYKAKAAAAA 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	63.4	300	2	Q9VFL4
2	45	63.4	463	2	Q9VFL4
3	45	63.4	707	2	Q9VFL4
4	43	60.6	312	1	RU22_DROME
5	43	60.6	312	2	Q9UANI
6	43	60.6	508	2	Q6QUT5
7	43	60.6	570	2	Q96M46
8	42	59.2	177	1	RL19_RHME
9	42	59.2	179	1	RL19_AGR15
10	42	59.2	181	1	RL19_RHLO
11	42	59.2	188	1	HXD8_CHICK
12	42	59.2	289	1	HXD8_MOUSE
13	42	59.2	289	2	Q81XZ1
14	42	59.2	290	1	HXD8_HUMAN
15	42	59.2	366	2	Q6FT73
16	42	59.2	395	2	Q6D7F3
17	41.5	58.5	189	2	Q7M495
18	41.5	58.5	189	2	Q7M496
19	41	57.7	165	2	Q64SE1
20	41	57.7	177	1	MSRA_LISIN
21	41	57.7	177	1	MSRA_LISIN
22	41	57.7	177	1	MSRA_LISIN
23	41	57.7	254	1	143A_ARATH
24	41	57.7	274	2	Q8T4F3
25	41	57.7	274	2	Q9VFL3
26	41	57.7	274	2	Q6UK87
27	41	57.7	316	2	Q8A8P1
28	41	57.7	432	2	Q8IR58
29	41	57.7	551	1	CAIX_PEA
30	41	57.7	574	2	Q8SKM8
31	41	57.7	607	2	Q9W327

RESULT 1	ID	Q9VFL4	PRELIMINARY;	PRT;	300 AA.
AC	Q9VFL4				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)			
DE	CG14840-PA (AT18408P).				
GN	ORFNames=CG14840;				
OS	Drosophila melanogaster (fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;				
RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,				
RA	Abriil J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Dubin K.J., Evangelista C.C., Ferraz C., Fiertera S., Fleischmann W.,				
RA	Fowler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,				
RA	Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Li X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,				
RA	Palazzo M., Pittman G.S., Pan S., Pollard V., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,				
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,				
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,				
RA	Svirskas R., Tector C., Turner C., Venter B., Venter A.H., Wang X.,				
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,				
RA	Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao O.A., Ye J.,				
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang M., Zhang Q., Zheng L.,				
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;				
RT	"The genome sequence of Drosophila melanogaster."				

ALIGNMENTS

32	41	57.7	847	2	Q7SC23
33	41	57.7	1271	2	Q7K705
34	41	57.7	1878	2	Q6BMT1
35	41	57.7	1885	1	FAS2_CANAL
36	41	57.7	2139	2	Q9UIR8
37	40	56.3	73	1	PHD_BPPI
38	40	56.3	73	2	Q7XA04
39	40	56.3	153	2	Q7XV75
40	40	56.3	177	2	Q8LQ30
41	40	56.3	281	2	Q7X2V5
42	40	56.3	289	2	Q71W13
43	40	56.3	377	2	P78866
44	40	56.3	404	2	Q7F9Q4
45	40	56.3	413	2	Q835A1
					Q835A1 shigella fl

Science 287:2185-2195(2000).

[2] SEQUENCE FROM N.A.
 RP MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3] SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.F.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[5] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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[6] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
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 RA Lewis S.E.,
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[9] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.F.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
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[10] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
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 RA Lewis S.E.,
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 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[11] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
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 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[12] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
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 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[13] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
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 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.F.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[14] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.F.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

01-MAY-2000 (T-EMBLrel. 13, Created)
 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE C66301-PA.
 GN ORFNames=C66301;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neuroptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baller R.M., Basu A., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klump D., Lai Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Stryer E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodger, Motley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yah R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).

[2] SEQUENCE FROM N.A.
 RP MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3] SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4] SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.F.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03805; AAF57947.2; -
 DR IntAct: Q9V7U6; -
 DR FlyBase; FBgn0034161; CG6301.
 DR InterPro: IPR007999; DUF745.
 DR Pfam; PF05335; DUF745; 1.
 SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEF6EBC9 CRC64;
 Query Match 63.4%; Score 45; DB 2; Length 463;
 Best Local Similarity 71.4%; Pred. No. 44;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 EKAKYKAYKAAAA 14
 Db 275 EKTQAAKAYKAAACAA 288

RESULT 3
 ID 064CP3 PRELIMINARY; PRT; 707 AA.
 AC 064CP3;
 DT 25-OCT-2004 (TREMBlrel. 28; Created)
 DT 25-OCT-2004 (TREMBlrel. 28; Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28; Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=GZ1D1_21;
 OS Uncultured archaean GZfos1D1.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=286721;
 RX PubMed=15353801.
 RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
 RA Richardson P.M., Delong E.F.;
 RT "Reverse metagenomics: testing the hypothesis with environmental
 RT genomes.";
 RL Science 305:1457-1462(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY14833; AAU82834.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 707 AA; 78670 MW; 104FE803BA51973D CRC64;
 Query Match 63.4%; Score 45; DB 2; Length 707;
 Best Local Similarity 73.3%; Pred. No. 66;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 EKAKYKAYKAAAA 15
 Db 645 EKTQAAKAYKAAAA 659

RESULT 4
 ID RL22 DROME STANDARD; PRT; 299 AA.
 AC P50887; O9V3X9;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 25-JAN-2005 (Rel. 46; Last annotation update)
 DE 60S ribosomal protein L22.
 GN Name=Rpl22; ORFNames=CG7434;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glover C.V.C., Bidwai A.P., Zhao W.F.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abdl J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brooksstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshirei A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton W., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

[4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Oregon-R.
 RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Bartell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
 RA Minana S., Gloux S., Lelaure V., Mottier S., Galbert F., Borova D.,
 RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papadimitrakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlatsou A., Henderson N.S.,
 RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster";
 RL Science 287:2220-2222(2000).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L22e family.
 CC -----
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 CC -----
 DR EMBL; U42587; AAB17433.1; -;
 DR EMBL; AE003418; AAF45546.1; -;
 DR EMBL; AL132792; CAB60023.1; -;
 DR Inctact; P50887; -;
 DR FLYBASE; FBgn0015288; RPL22.
 DR InterPro; IPR002671; Ribosomal_L22e.
 DR Pfam; PF01776; Ribosomal_L22e; 1.
 DR ProDom; PD007306; Ribosomal_L22e; 1.
 KW Ribosomal protein.
 FT DOMAIN 24 31 Poly-Ala.
 FT DOMAIN 46 50 Poly-Ala.
 FT DOMAIN 65 70 Poly-Ala.
 FT DOMAIN 93 98 Poly-Ala.
 FT DOMAIN 103 112 Poly-Ala.
 FT DOMAIN 136 152 Poly-Ala.
 FT DOMAIN 185 188 Poly-Lys.
 FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).
 SQ SEQUENCE 299 AA; 30610 MW; 46A9905610B4EB0 CRC64;
 Query Match 60.6%; Score 43; DB 1; Length 299;
 Best Local Similarity 73.3%; Pred. No. 63;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EKAKYENYKAAAAA 15
 DB 36 EKPKAAKAPAAAAA 50
 RESULT 5
 Q9UN1 PRELIMINARY; PRT; 312 AA.
 AC Q9UN1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein L22 (Fragment).
 GN Name=RPL22; Synonyms=rp122;
 OS Drosophila melanogaster (fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9912306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
 RA Koyama Y., Katagiri S., Hana S., Uchida K., Miwa M.;

RT "Poly(Adp-ribose) polymerase interacts with novel Drosophila ribosomal
 RT proteins, l22 and l23a, with unique histone-like amino-terminal
 RT extensions";
 RL Gene 226:339-345(1999).
 DR EMBL; AF080131; AAD19341.1; -;
 DR FLYBASE; FBgn0015288; RPL22.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR002671; Ribosomal_L22e.
 DR Pfam; PF01776; Ribosomal_L22e; 1.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
 Query Match 60.6%; Score 43; DB 2; Length 312;
 Best Local Similarity 73.3%; Pred. No. 65;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EKAKYENYKAAAAA 15
 DB 49 EKPKAAKAPAAAAA 63
 RESULT 6
 Q6QUT5 PRELIMINARY; PRT; 508 AA.
 AC Q6QUT5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PS2.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OC NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22243;
 RX PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;
 RA Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tausch A.,
 RA Puhler A., Kalinowski J.;
 RT "Classification of hyper-variable Corynebacterium glutamicum surface-
 RT layer proteins by sequence analyses and atomic force microscopy";
 RL J. Biotechnol. 112:177-193(2004).
 RU EMBL; AY525006; AAS20307.1; -;
 SQ SEQUENCE 508 AA; 55416 MW; B28137E469228581 CRC64;
 Query Match 60.6%; Score 43; DB 2; Length 508;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EKAKYENYKAAAAA 15
 DB 104 EQAAYEAFERARARA 118
 RESULT 7
 Q96M46 PRELIMINARY; PRT; 570 AA.
 AC Q96M46;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ32830.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;

CC aminoacyl-tRNA binding site (By similarity).

CC -1- SIMILARITY: Belongs to the ribosomal protein L19p family.

CC -----

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CC -----

CC EMBL: AE009216; ALA43684.1; -

CC EMBL: AE008183; AAK8423.1; -

CC PIR: AF2908; AF2908.

CC PIR: P97683; P97683.

CC HAMAP: MF_00402; -; 1.

CC InterPro: IPR001857; Ribosomal_L19.

CC Pfam: PF01245; Ribosomal_L19; 1.

CC PRINTS: PR00061; RIBOSOMALL19.

CC ProDom: PD002979; Ribosomal_L19; 1.

CC TIGRFAMs: TIGR01024; rplS_bact; 1.

CC PROSITE: PS01015; RIBOSOMAL_L19; 1.

CC DR PROSITE: PS01015; RIBOSOMAL_L19; 1.

CC KM COMPLETE proteome; Ribosomal protein.

CC SQ SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

Query Match 59.2%; Score 42; DB 1; Length 179;

Best Local Similarity 66.7%; Pred. No. 56;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKTEAYKAAAAA 15

DB 137 EKARLEAEKVAQA 151

RESULT 10

RL19_RHIL0 STANDARD; PRT; 181 AA.

AC P58168;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE 50S ribosomal protein L19.

GN Name=rplS; OrderedLocNames=rll12483;

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

OR [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF30309; PubMed=11214968;

RA MEDLINE=21082930; Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Kawanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kibida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuo A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti."

RL DNA Res. 7:331-338 (2000).

CC -1- FUNCTION: This protein is located at the 30S-50S ribosomal subunit

CC interface and may play a role in the structure and function of the

CC aminoacyl-tRNA binding site (By similarity).

CC -1- SIMILARITY: Belongs to the ribosomal protein L19p family.

CC -----

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CC -----

CC EMBL: AP003003; BAB50976.1; -

DR HAMAP: MF_00402; -; 1.

DR InterPro: IPR001857; Ribosomal_L19.

DR Pfam: PF01245; Ribosomal_L19; 1.

DR PRINTS: PR00061; RIBOSOMALL19.

DR ProDom: PD002979; Ribosomal_L19; 1.

DR TIGRFAMs: TIGR01024; rplS_bact; 1.

DR PROSITE: PS01015; RIBOSOMAL_L19; 1.

DR KM COMPLETE proteome; Ribosomal protein.

DR SQ SEQUENCE 181 AA; 19927 MW; AE19D6593A9E835 CRC64;

Query Match 59.2%; Score 42; DB 1; Length 181;

Best Local Similarity 66.7%; Pred. No. 57;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKTEAYKAAAAA 15

DB 136 EKARLEAEKVAQA 150

RESULT 11

HXB8_CHICK STANDARD; PRT; 188 AA.

AC P23459;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Homeobox protein Hox-D8 (Chox-M).

GN Name=HoxD8; Synonyms=CHOX-M;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

OR [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=91238215; PubMed=1674560;

RA Crompton M.R., McGregor A.D., Goodwin G.H.;

RT "cDNA cloning of a homeobox-containing gene expressed in avian

RT myeloblastic virus-transformed chicken monoblastic leukaemia cells.;"

RL Leukemia 5:357-360 (1991).

CC -1- FUNCTION: Sequence-specific transcription factor which is part of

CC a developmental regulatory system that provides cells with

CC specific positional identities on the anterior-posterior axis.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: Belongs to the Anp homeobox family.

CC -1- SIMILARITY: Contains 1 homeobox domain.

CC -----

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CC -----

CC EMBL: X57158; CAA40445.1; -

CC PIR: I50145; I50145.

CC HSSP: P02833; 9ANT.

CC TRANSFAC: T01754; -

CC InterPro: IPR001827; Antennapedia.

CC InterPro: IPR001356; Homeobox.

CC InterPro: IPR009057; Homeodomain_1ike.

CC InterPro: IPR000047; HTH_1andrepresr.

CC Pfam: PF00046; Homeobox; 1.

CC PRINTS: PR00025; ANTENNAPEDIA.

CC PRINTS: PR00024; HOMEOBOX.

CC PRINTS: PR00031; HTHREPRESSR.

CC ProDom: PD000010; Homeobox; 1.

CC SMART: SM00389; HOX; 1.

CC PROSITE: PS00032; ANTENNAPEDIA; 1.

CC PROSITE: PS00027; HOMEOBOX; 1; 1.

CC PROSITE: PS00071; HOMEOBOX_2; 1.

CC KM Developmental protein; DNA-binding; Homeobox; Nuclear protein;


```

KW Transcription regulation.
FT PIR: A43562; A43605.
FT PIR: S16177; A41605.
FT HSSP; P02833; 9ANT.
FT TRANSFAC; T01426; -.
FT MGD; MGI:96209; Hoxd8.
FT InterPro; IPR001827; Antennapedia.
FT InterPro; IPR001356; Homeobox.
FT InterPro; IPR009057; Homeobox_1.
FT Pfam; PF00046; Homeobox; 1.
FT PRINTS; PR00025; ANTENNAPEDIA.
FT PRINTS; PR00024; HOMEOBOX.
FT ProDom; PD000010; Homeobox; 1.
FT SMART; SM00389; Hox; 1.
FT PROSITE; PS00032; ANTENNAPEDIA; 1.
FT PROSITE; PS00027; HOMEOBOX_1; 1.
FT PROSITE; PS50071; HOMEOBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 28 Poly-Ala.
FT P23463; Gly/Pro-rich.
FT AC P23463; Poly-Pro.
FT DT 01-NOV-1991 (Rel. 20, Created) Antp-type hexapeptide.
FT DT 01-JUL-1993 (Rel. 26, Last sequence update) Homeobox.
FT DT 05-JUL-2004 (Rel. 44, Last annotation update) Homeobox.
DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).
OS Name=Hoxd8; Synonyms=Hox-4.3, Hoxd-8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91209232; PubMed=1982431;
RA Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,
RT Falkenstein H., Duboule D.;
RT "Primary structure and embryonic expression pattern of the mouse Hox-
RT 4.3 homeobox gene.";
RL Development 110:733-745 (1990).
RN [2]
RP SEQUENCE OF 191-289 FROM N.A.
RX MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;
RA Sadouli R., Featherstone M.;
RT "Sequence analysis of the homeobox-containing exon of the murine Hox-
RT 4.3 homeogene.";
RL Biochim. Biophys. Acta 1089:259-261 (1991).
RN [3]
RP SEQUENCE OF 195-254 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710 (1991).
RN [4]
RP SEQUENCE OF 192-260 FROM N.A.
RX MEDLINE=92212934; PubMed=1348361;
RA Nazareli A., Kim Y., Nirenberg M.;
RT "Hox-1.1 and Hox-4.9 homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887 (1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56561; CAA39911.1; -.
DR EMBL; M87803; AAA37852.1; -.

```

```

DR PIR; A43562; A43605.
DR PIR; S16177; A41605.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T01426; -.
DR MGD; MGI:96209; Hoxd8.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeobox_1.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 28 Poly-Ala.
FT P23463; Gly/Pro-rich.
FT AC P23463; Poly-Pro.
FT DT 01-NOV-1991 (Rel. 20, Created) Antp-type hexapeptide.
FT DT 01-JUL-1993 (Rel. 26, Last sequence update) Homeobox.
FT DT 05-JUL-2004 (Rel. 44, Last annotation update) Homeobox.
DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).
OS Name=Hoxd8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91209232; PubMed=1982431;
RA Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,
RT Falkenstein H., Duboule D.;
RT "Primary structure and embryonic expression pattern of the mouse Hox-
RT 4.3 homeobox gene.";
RL Development 110:733-745 (1990).
RN [2]
RP SEQUENCE OF 191-289 FROM N.A.
RX MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;
RA Sadouli R., Featherstone M.;
RT "Sequence analysis of the homeobox-containing exon of the murine Hox-
RT 4.3 homeogene.";
RL Biochim. Biophys. Acta 1089:259-261 (1991).
RN [3]
RP SEQUENCE OF 195-254 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710 (1991).
RN [4]
RP SEQUENCE OF 192-260 FROM N.A.
RX MEDLINE=92212934; PubMed=1348361;
RA Nazareli A., Kim Y., Nirenberg M.;
RT "Hox-1.1 and Hox-4.9 homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887 (1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56561; CAA39911.1; -.
DR EMBL; M87803; AAA37852.1; -.

```

RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: BC038709; AF38709.1; -.
 DR HSSP: P02833; 9ANT.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001827; Antennapedia.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR009057; Homeodomain_1like.
 DR Pfam: PF00046; Homeobox; 1.
 DR PRINTS: PR00025; ANTENNAPEDIA.
 DR PRINTS: PR00024; HOMEBOX.
 DR PRODOM: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; UNKNOWN_1.
 DR PROSITE: PS00027; HOMEBOX 1; 1.
 DR PROSITE: PS50071; HOMEBOX 2; 1.
 KM DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 289 AA; 31839 MW; 4C2621085174B447 CRC64;
 Query Match 59.2%; Score 42; DB 2; Length 289;
 Best Local Similarity 81.8%; Pred. No. 89;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 YEAYKAAAAA 15
 DB 10 YSKYKAAAAA 20
 RESULT 14;
 HXD8 HUMAN STANDARD; PRT; 290 AA.
 AC P13378;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Homeobox protein Hox-D8 (Hox-5.4).
 GN Name=HoxD8; Synonyms=HOX4E;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Birren B., Linton L., Nusbaum C., Lander E.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kosaki K., Kosaki R., Suzuki T., Yoshinashi H., Saeki K., Matsuo N.;
 RT "A complete mutation analysis panel of human HOX genes";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 193-287 FROM N.A.
 RX MEDLINE=89306602; Pubmed=2568311;
 RA Oliver G., Stidell N., Fiske N., Heinzmann C., Mohandas T.,
 RA Sparkes R.S., de Robertis E.M.;
 RT "Complementary homeo protein gradients in developing limb buds";
 RL Genes Dev. 3:641-650(1989).
 CC -1- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the Antp homeobox family.
 CC -1- SIMILARITY: Contains 1 homeobox domain.
 CC -----
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 CC -----
 DR EMBL: AC009336; -; NOT ANNOTATED_CDS.
 DR EMBL: AY014304; AF42152.1; -.
 DR EMBL: AY014303; AF42152.1; JOINED.
 DR EMBL: X15507; CA33529.1; -.
 DR PIR: B32830; B32830.
 DR HSSP: P02833; 9ANT.
 DR TRANSFAC: T03332; -.
 DR GeneW: HGNC:5139; HOXD8.
 DR MIM: 142985; -.
 DR GO: GO:0005634; C:nucleus; NAS.
 DR GO: GO:0003700; P:transcription factor activity; NAS.
 DR GO: GO:0006355; P:determination of anterior/posterior axis, e...; NAS.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro: IPR001827; Antennapedia.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR009057; Homeodomain_1like.
 DR Pfam: PF00046; Homeobox; 1.
 DR PRINTS: PR00025; ANTENNAPEDIA.
 DR PRINTS: PR00024; HOMEBOX.
 DR PRODOM: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; 1.
 DR PROSITE: PS00027; HOMEBOX 1; 1.
 DR PROSITE: PS50071; HOMEBOX 2; 1.
 KM Developmental protein; DNA-binding; Homeobox; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 15 23 Poly-Ala.
 FT DOMAIN 45 50 Poly-Ala.
 FT DOMAIN 109 123 Poly-Pro.
 FT DNA BIND 197 256 Homeobox.
 FT CONFLICT 287 287 G -> A (in Ref. 3).
 SQ SEQUENCE 290 AA; 31910 MW; 75FF95A73E2AA85F CRC64;
 Query Match 59.2%; Score 42; DB 1; Length 290;
 Best Local Similarity 81.8%; Pred. No. 89;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 YEAYKAAAAA 15
 DB 10 YSKYKAAAAA 20
 RESULT 15
 ID Q6FT73 PRELIMINARY; PRT; 366 AA.
 AC Q6FT73;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similar to sp|P40319 Saccharomyces cerevisiae YJR372w SUR4 sterol
 DE isomerase.
 GN ORFNames=CAGL0G048519;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissame A., Boyer J., Cattolico L., Confalonieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekai F., Wesolowski-Louvel M., Weschof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 DR EMBL, CR380953; CAG59498.1; -.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0016853; F:Isomerase activity; IEA.
 DR InterPro; IPR02076; GNS1_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 KW Isomerase.
 SQ SEQUENCE 366 AA; 41202 MW; 29E7E159FF08BB76 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 366;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKATYEAAYKAAAAA 15
 :||:|||||:
 Db 335 KKAKEKAAYKAAAAA 349

Search completed: February 26, 2005, 23:55:37
 Job time : 70.2041 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 97.1327 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583a-89
Perfect score: 93
Sequence: 1 APEKAKYKAYKAAAAAPA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seque, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	19	5	ABP52295 HLA-DR2 m
2	82	88.2	17	5	ABP52294 HLA-DR2 m
3	82	88.2	17	5	ABP52296 HLA-DR2 m
4	73	78.5	17	5	ABP52303 HLA-DR2 m
5	71	76.3	15	5	ABP52271 HLA-DR2 m
6	71	76.3	15	5	ABP52298 HLA-DR2 m
7	69	74.2	17	5	ABP52302 HLA-DR2 m
8	65	69.9	15	5	ABP52270 HLA-DR2 m
9	63	67.7	15	5	ABP52301 HLA-DR2 m
10	61	65.6	15	5	ABP52291 HLA-DR2 m
11	61	65.6	15	5	ABP52263 HLA-DR2 m
12	60	64.5	15	5	ABP52272 HLA-DR2 m
13	59	63.4	15	5	ABP52259 HLA-DR2 m
14	59	63.4	15	5	ABP52257 HLA-DR2 m
15	57	61.3	15	5	ABP52297 HLA-DR2 m
16	56	60.2	15	5	ABP52253 HLA-DR2 m
17	56	60.2	15	5	ABP52251 HLA-DR2 m
18	55	59.1	15	5	ABP52239 HLA-DR2 m
19	55	59.1	15	5	ABP52290 HLA-DR2 m
20	55	59.1	15	5	ABP52261 HLA-DR2 m
21	55	59.1	15	5	ABP52244 HLA-DR2 m
22	55	59.1	15	5	ABP52292 HLA-DR2 m
23	55	59.1	15	5	ABP52269 HLA-DR2 m
24	55	59.1	15	5	ABP52262 HLA-DR2 m
25	54	58.1	15	5	ABP52264 HLA-DR2 m

26	54	58.1	15	5	ABP52267 HLA-DR2 m
27	54	58.1	15	5	ABP52236 HLA-DR2 m
28	54	58.1	15	5	ABP52295 HLA-DR2 m
29	53	57.0	15	5	ABP52299 HLA-DR2 m
30	52	55.9	15	5	ABP52265 HLA-DR2 m
31	51	54.8	15	5	ABP52254 HLA-DR2 m
32	51	54.8	15	5	ABP52255 HLA-DR2 m
33	51	54.8	15	5	ABP52240 HLA-DR2 m
34	51	54.8	15	5	ABP52241 HLA-DR2 m
35	51	54.8	15	5	ABP52304 HLA-DR2 m
36	51	54.8	15	5	ABP52248 HLA-DR2 m
37	51	54.8	15	5	ABP52249 HLA-DR2 m
38	50	53.8	15	5	ABP52232 HLA-DR2 m
39	50	53.8	15	5	ABP52268 HLA-DR2 m
40	50	53.8	15	5	ABP52231 HLA-DR2 m
41	50	53.8	15	5	AD455549 Human pro
42	50	53.8	15	5	AD455549 Human pro
43	49	52.7	15	5	AD455549 Human pro
44	49	52.7	15	5	AD455549 Human pro
45	48	51.6	15	3	AAY58982 Copeptide

ALIGNMENTS

RESULT 1
ABP52295
ID ABP52295 standard; peptide; 19 AA.
AC
XX ABP52295;
XX
XX 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX immune response; anti-inflammatory; neuroprotective; proliferation;
XX MHC class II protein inhibitor; demyelinating disease; inhibition;
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
XX Synthetic.
XX OS
XX PN W0200259143-A2.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-US002071.
XX PK 24-JAN-2001; 2001US-0263569P.
XX PA (HARD) HARVARD COLLEGE.
XX PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX demyelinating disease, e.g. multiple sclerosis, or post-viral
XX encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX residues. The complex of the peptide with a major histocompatibility
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX immune response. (I) has anti-inflammatory and neuroprotective activities,
XX and can be used as a MHC class II protein inhibitor. The compositions
XX comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX Sequence 19 AA:
 SQ
 Query Match 100.0%; Score 93; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APEKAKYEAYKAAAAAPA 19
 DB 1 APEKAKYEAYKAAAAAPA 19
 RESULT 2
 ABP52294 standard; peptide; 17 AA.
 ID ABP52294
 XX
 AC ABP52294;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; anti-inflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX WO200259143-A2.
 XX
 PN 01-AUG-2002.
 XX
 PD 24-JAN-2002; 2002WO-US002071.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has anti-inflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX

SQ Sequence 17 AA;
 Query Match 88.2%; Score 82; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APEKAKYEAYKAAAAAPA 17
 DB 1 APEKAKYEAYKAAAAAPA 17
 RESULT 3
 ABP52296 standard; peptide; 17 AA.
 ID ABP52296
 XX
 AC ABP52296;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; anti-inflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX WO200259143-A2.
 XX
 PN 01-AUG-2002.
 XX
 PD 24-JAN-2002; 2002WO-US002071.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
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 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
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 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
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 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 AA;
 Query Match 88.2%; Score 82; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EKAKYEAYKAAAAAPA 19

Db 1 EKAKEAYKAAAAA 17

RESULT 4
ABP52303
ID ABP52303 standard; peptide; 17 AA.

AC ABP52303;
DE 16-OCT-2002 (first entry)
XX HLA-DR2 molecule binding peptide SEQ ID NO:97.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.
XX WO200259143-A2.

XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-US002071.
XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 17 AA;

Query Match 78.5%; Score 73; DB 5; Length 17;
Best Local Similarity 88.2%; Pred. No. 0.00022;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
ID 1 APEKAKYEAYKAAAAA 17

RESULT 5
ABP52271
ID ABP52271 standard; peptide; 15 AA.

XX ABP52271;

AC 16-OCT-2002 (first entry)
XX HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.
XX WO200259143-A2.

XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-US002071.
XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 15 AA;

Query Match 76.3%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
ID 3 EKAKEAYKAAAAA 17

RESULT 6
ABP52298
ID ABP52298 standard; peptide; 15 AA.

AC ABP52298;
DE 16-OCT-2002 (first entry)

XX HLA-DR2 molecule binding peptide SEQ ID NO:92.

PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX WPI; 2002-608439/65.
 DR
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 69.9%; Score 65; DB 5; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.0034;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EKAKYEAYKAAAAA 17
 Db 1 EAKYEAYKAAAAA 15
 XX
 RESULT 9
 ABP52301
 ID ABP52301 standard; peptide: 15 AA.
 XX
 AC ABP52301;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:95.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;

XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 67.7%; Score 63; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0069;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EKAKYEAYKAAAAA 17
 Db 1 EAKYEAYKAAAAA 15
 XX
 RESULT 10
 ABP52291
 ID ABP52291 standard; peptide: 15 AA.
 XX
 AC ABP52291;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX	Claim 28; Page 39; 54pp; English.
PS	
XX	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	demyelinating condition, and a side effect of administering an anti-
CC	tumour neurotoxic factor agents. The peptide further inhibits proliferation
CC	of autacantigen-specific HLA-DR2-restricted T cell clones. AB52207 to
CC	AB522305 represent peptides used in the exemplification of the present
CC	invention
XX	
XX	Sequence 15 AA;
XX	
XX	Query Match 65.6%; Score 61; DB 5; Length 15;
XX	Best Local Similarity 86.7%; Pred. No. 0.014;
XX	Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	3 EKAKYEAYKAAAPAA 17
Db	1 EKPKTEAYKAAAPAA 15
XX	
XX	RESULT 11
XX	ABP52263
XX	ID ABP52263 standard; peptide; 15 AA.
XX	ABP52263;
XX	16-OCT-2002 (first entry)
DE	HLA-DR2 molecule binding peptide SEQ ID NO:57.
XX	
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW	HLA-DR; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW	immune response; antiinflammatory; neuroprotective; proliferation;
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW	anti-tumour necrosis factor agent.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
PF	24-JAN-2002; 2002MO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
FI	Strominger JL, Fridkis-Hareli M;
DR	WPI; 2002-608439/65.
XX	
PT	New compositions comprising synthetic peptides in complex with a major
PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral
PT	encephalomyelitis.
XX	
PS	Example 1; Page 33; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an

	immune response. (I) has antiinflammatory and neuroprotective activities
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	demyelinating condition, and a side effect of administering an anti-
CC	tumour necrosis factor agents. The peptide further inhibits proliferation
CC	of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC	ABP52305 represent peptides used in the exemplification of the present
CC	invention
XX	
SQ	Sequence 15 AA;
	Query Match 65.6%; Score 61; DB 5; Length 15;
	Best Local Similarity 86.7%; Pred. No. 0.014;
	Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy	3 EKAKTEAYKAAAAA 17 : 1 EAAKYAAVKAAMAAA 15
Dd	
	RESULT 12
ID	ABP52272
XX	ID ABP52272 standard; peptide; 15 AA.
AC	ABP52272;
XX	
DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:66.
KM	Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
Pf	24-JAN-2002; 2002WO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	Strominger JL, Fridkis-Hareli M;
XX	
DR	WPI; 2002-608439/65.
XX	
PT	New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HUADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
PT	
XX	
PS	Claim 28; Page 39; 5app; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti- tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 64.5%; Score 60; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
 DB 1 EAKKEAYKAAAAA 15

RESULT 13

ABP52259 standard; peptide; 15 AA.

ID ABP52259 standard; peptide; 15 AA.
 AC ABP52259;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:53.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 PT
 PS Example 1; Page 33; 54pp; English.
 XX

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 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
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 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
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 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 63.4%; Score 59; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.029;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
 DB 1 EKAKEAYKAAAAA 15

RESULT 14

ABP52257 standard; peptide; 15 AA.

ID ABP52257 standard; peptide; 15 AA.
 AC ABP52257;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 PD 01-AUG-2002.
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 PT
 PS Example 1; Page 32; 54pp; English.
 XX

CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 63.4%; Score 59; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.029;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
 DB 1 EKAKEAYKAAAAA 15

```

RESULT 15
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

```

Query Match 61.3%; Score 57; DB 5; Length 15;
 Best Local Similarity 80.0%; Pred. No. 0.058;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY      3 EKAKYEAYKAAAAA 17
      |||:|||||||
Db      1 EKPKYEAYKAAAAA 15

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Search completed: February 26, 2005, 23:48:22
 Job time : 97.1327 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 25.398 Seconds
(without alignments)
55.844 Million cell updates/sec

Title: US-10-056-583A-89

Perfect score: 93
Sequence: 1 APEKAYEAKAAAAAPA 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/5B COMB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	51.6	118	4 US-09-101-751A-46	Sequence 46, Appl
2	47.5	51.1	219	4 US-09-902-540-1623	Sequence 1623, A
3	47	50.5	612	4 US-09-252-991A-25727	Sequence 25727, A
4	45	48.4	137	4 US-10-081-817A-30	Sequence 30, Appl
5	45	48.4	595	4 US-10-052-092-31	Sequence 31, Appl
6	45	48.4	1001	4 US-09-248-796A-18658	Sequence 18658, A
7	44.5	47.8	324	4 US-09-248-796A-17156	Sequence 17156, A
8	44.5	47.8	596	4 US-08-836-620A-16	Sequence 16, Appl
9	44	47.3	405	4 US-09-328-352-4239	Sequence 4239, Ap
10	43	46.2	55	4 US-09-902-540-9849	Sequence 9849, Ap
11	43	46.2	162	4 US-09-732-210-1445	Sequence 1445, Ap
12	43	46.2	172	4 US-09-902-540-13256	Sequence 13256, A
13	43	46.2	419	4 US-09-489-039A-13260	Sequence 13260, A
14	42	45.2	13	5 PCT-US95-04121-38	Sequence 38, Appl
15	42	45.2	38	3 US-09-117-121-16	Sequence 16, Appl
16	42	45.2	38	3 US-09-117-121-24	Sequence 24, Appl
17	42	45.2	38	4 US-09-344-529-5	Sequence 5, Appl
18	42	45.2	136	4 US-09-732-210-630	Sequence 630, App
19	42	45.2	136	4 US-09-711-164-303	Sequence 303, App
20	42	45.2	136	4 US-09-492-709A-385	Sequence 385, App
21	42	45.2	178	4 US-09-252-991A-20280	Sequence 20280, A
22	42	45.2	189	4 US-09-902-540-12588	Sequence 12588, A
23	42	45.2	190	4 US-09-902-540-14713	Sequence 14713, A
24	42	45.2	220	4 US-09-902-540-9904	Sequence 9904, A
25	42	45.2	273	4 US-09-910-430-34	Sequence 34, Appl
26	42	45.2	318	4 US-09-270-767-45996	Sequence 45996, A
27	42	45.2	519	4 US-09-902-540-15378	Sequence 15378, A

28	42	45.2	538	4 US-09-616-289-43	Sequence 43, Appl
29	41.5	44.6	1156	4 US-09-902-540-15564	Sequence 15564, A
30	41	44.1	54	3 US-09-117-121-30	Sequence 30, Appl
31	41	44.1	56	4 US-09-405-743A-3	Sequence 3, Appl
32	41	44.1	56	4 US-09-816-989A-3	Sequence 3, Appl
33	41	44.1	77	4 US-09-405-743A-5	Sequence 5, Appl
34	41	44.1	77	4 US-09-816-989A-5	Sequence 5, Appl
35	41	44.1	86	4 US-09-405-743A-6	Sequence 6, Appl
36	41	44.1	86	4 US-09-816-989A-6	Sequence 6, Appl
37	41	44.1	102	4 US-09-101-751A-90	Sequence 90, Appl
38	41	44.1	166	4 US-09-252-991A-22139	Sequence 22139, A
39	41	44.1	218	4 US-09-101-751A-48	Sequence 48, Appl
40	41	44.1	245	4 US-09-902-540-12314	Sequence 12314, A
41	41	44.1	287	3 US-09-105-697-7	Sequence 7, Appl
42	41	44.1	287	3 US-09-105-697-8	Sequence 8, Appl
43	41	44.1	288	3 US-09-105-697-3	Sequence 3, Appl
44	41	44.1	291	3 US-09-105-697-4	Sequence 4, Appl
45	41	44.1	291	3 US-09-105-697-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-101-751A-46
; Sequence 46, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGHT, DOUGLAS E.
; TITLE OR INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
US-09-101-751A-46
Query Match 51.6%; Score 48; DB 4; Length 118;
Best Local Similarity 61.1%; Pred. NO. 2;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db 68 PEKAYEAKAAAAAPA 19
2 PEKAYEAKAAAAAPA 19
US-09-902-540-16623
; Sequence 16623, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```

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; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16623
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-16623

Query Match          51.1%; Score 47.5; DB 4; Length 219;
Best Local Similarity 68.4%; Pred. No. 4.8;
Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      1 APEKAYEAYKAAAP 19
Db      189 ABEKARAT-FAAATAAP 206

RESULT 3
US-09-252-991A-25727
; Sequence 25727; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25727
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-25727

Query Match          50.5%; Score 47; DB 4; Length 612;
Best Local Similarity 44.4%; Pred. No. 18;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 PEKAYEAYKAAAP 19
Db      206 PDPAYRAMRGASAP 223

RESULT 4
US-10-081-817A-30
; Sequence 30; Application US/10081817A
; Patent No. 6815166
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Porter, Dale
; APPLICANT: Sgroi, Dennis
; APPLICANT: Krop, Ian
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 00530-094001
; CURRENT APPLICATION NUMBER: US/10/081,817A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/270,973
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 30
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-081-817A-30

Query Match          48.4%; Score 45; DB 4; Length 137;
Best Local Similarity 63.2%; Pred. No. 7.1;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 APEKAYEAYKAAAP 19
Db      75 APVAAATPVAAYAAP 93

RESULT 5
US-10-052-092-31
; Sequence 31; Application US/10052092
; Patent No. 6821732
; GENERAL INFORMATION:
; APPLICANT: Fugua, Suzanne
; APPLICANT: Alired, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeut
; FILE REFERENCE: P02102US2
; CURRENT APPLICATION NUMBER: US/10/052,092
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,990
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/304,018
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 595
; TYPE: PRT
; ORGANISM: pig
; US-10-052-092-31

Query Match          48.4%; Score 45; DB 4; Length 595;
Best Local Similarity 58.8%; Pred. No. 36;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 PEKAYEAYKAAAP 18
Db      55 PEGAYDPNAAASAP 71

RESULT 6
US-09-248-796A-18658
; Sequence 18658; Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18658
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
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US-09-248-796A-18658

Query Match 48.4%; Score 45; DB 4; Length 1001;

Best Local Similarity 75.0%; Pred. No. 64;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 KAKYAYKAAAAAPA 19

Db 818 KAKEAEAAAAAAA 833

RESULT 7

US-09-248-796A-17156

Sequence 17156, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

NUMBER OF SEQ ID NOS: 1998-08-13

SEQ ID NO 17156

LENGTH: 324

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-17156

Query Match 47.8%; Score 44.5; DB 4; Length 324;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 12; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 1 APEKAYEAYKAAAAAP 18

Db 157 APEKAE--SAPAAP 171

RESULT 8

US-08-836-620A-16

Sequence 16, Application US/08836620A

Patent No. 5958710

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Orphan receptor

NUMBER OF SEQUENCES: 19

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,620A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP96/03933

FILING DATE:

APPLICATION NUMBER: GB 9518272.1

FILING DATE: 08-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9605550.4

FILING DATE: 15-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9607532.0

FILING DATE: 11-APR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9609576.5

FILING DATE: 08-MAY-1996

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 596 amino acids

TYPE: amino acid

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: Rattus rattus

US-08-836-620A-16

Query Match 47.8%; Score 44.5; DB 2; Length 596;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 2 PEKAYEAYKAAAAAPA 19

Db 55 PEKAYE-FVAAAAAAA 71

RESULT 9

US-09-328-352-4239

Sequence 4239, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: C99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4239

LENGTH: 405

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4239

Query Match 47.3%; Score 44; DB 4; Length 405;

Best Local Similarity 66.7%; Pred. No. 34;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AKYAYKAAAAAPA 19

Db 81 AOFAGAGAAAAAPA 95

RESULT 10

US-09-902-540-9849

Sequence 9849, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 9849

LENGTH: 55

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-9849

Query Match 46.2%; Score 43; DB 4; Length 55;

Best Local Similarity 52.9%; Pred. No. 5.4;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EKAYEAYKAAAAAPA 19

Db 2 ETAREQAYVAAASACPA 18

RESULT 11
US-09-732-210-1445
Sequence 1445, Application US/09732210

Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mitanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Ronnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1445
LENGTH: 162
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-732-210-1445

Query Match 46.2%; Score 43; DB 4; Length 162;
Best Local Similarity 52.9%; Pred. No. 18;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 17
| : : : : : |
Db 97 APKPSKLEVFNALAA 113

RESULT 12
US-09-902-540-13256
Sequence 13256, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,893
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13256
LENGTH: 172
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-13256

Query Match 46.2%; Score 43; DB 4; Length 172;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 EAYKAAAAA 19
| : : : : : |
Db 160 EAQKAKAAAPA 171

RESULT 13
US-09-489-039A-13260
Sequence 13260, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.20040001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13260
LENGTH: 419
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13260

Query Match 46.2%; Score 43; DB 4; Length 419;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 19
| : : : : : |
Db 164 APAPAEKAPAAAPAA 182

RESULT 14
PCT-US95-04121-38
Sequence 38, Application PC/TUS9504121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-04121-38

Query Match 45.2%; Score 42; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 16;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAA 17
| : : : : : |
Db 1 AAYKAAKAAAAA 13

RESULT 15
US-09-117-121-16
Sequence 16, Application US/09117121
Patent No. 6307020
GENERAL INFORMATION:

APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 016252-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-117-121-16

Query Match 45.2%; Score 42; DB 3; Length 38;
Best Local Similarity 63.2%; Pred. No. 5.2;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 APEKAKYKAYKAAAPAA 19
DB 13 AAAPAAAEATGAAAKAAA 31

Search completed: February 26, 2005, 23:59:29
Job time : 26.398 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 67.8571 Seconds
(without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583A-89

Perfect score: 93

Sequence: 1 APEKXKYEAAYKAAAAAPA 19

Scoring table: BLOSUM62
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Searched: 1385339 seqs, 328044528 residues 1385339

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Post-processing: Minimum Match 0%

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9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubppaa/US09C_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubppaa/US10C_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	19	US-10-056-583-89	Sequence 89, App1
2	82	88.2	17	US-10-056-583-88	Sequence 88, App1
3	82	88.2	17	US-10-056-583-90	Sequence 90, App1
4	73	78.5	17	US-10-056-583-97	Sequence 97, App1
5	71	76.3	15	US-10-056-583-65	Sequence 65, App1
6	69	74.2	17	US-10-056-583-96	Sequence 96, App1
7	65	69.9	15	US-10-056-583-64	Sequence 64, App1
8	63	67.7	15	US-10-056-583-95	Sequence 95, App1
9	62	66.7	15	US-10-056-583-57	Sequence 57, App1
10	61	65.6	15	US-10-056-583-85	Sequence 85, App1
11	61	65.6	15	US-10-056-583-66	Sequence 66, App1
12	60	64.5	15	US-10-056-583-51	Sequence 51, App1
13	59	63.4	15	US-10-056-583-51	Sequence 51, App1

14	59	63.4	15	US-10-056-583-53	Sequence 53, App1
15	57	61.3	15	US-10-056-583-91	Sequence 91, App1
16	56	60.2	15	US-10-056-583-33	Sequence 33, App1
17	56	60.2	15	US-10-056-583-45	Sequence 45, App1
18	56	60.2	15	US-10-056-583-47	Sequence 47, App1
19	55	59.1	15	US-10-056-583-38	Sequence 38, App1
20	55	59.1	15	US-10-056-583-55	Sequence 55, App1
21	55	59.1	15	US-10-056-583-56	Sequence 56, App1
22	55	59.1	15	US-10-056-583-63	Sequence 63, App1
23	55	59.1	15	US-10-056-583-84	Sequence 84, App1
24	55	59.1	15	US-10-056-583-86	Sequence 86, App1
25	54	58.1	15	US-10-056-583-30	Sequence 30, App1
26	54	58.1	15	US-10-056-583-35	Sequence 35, App1
27	54	58.1	15	US-10-056-583-42	Sequence 42, App1
28	53	57.0	15	US-10-056-583-93	Sequence 93, App1
29	52	55.9	15	US-10-056-583-59	Sequence 59, App1
30	51	54.8	15	US-10-056-583-34	Sequence 34, App1
31	51	54.8	15	US-10-056-583-35	Sequence 35, App1
32	51	54.8	15	US-10-056-583-43	Sequence 43, App1
33	51	54.8	15	US-10-056-583-48	Sequence 48, App1
34	51	54.8	15	US-10-056-583-49	Sequence 49, App1
35	51	54.8	15	US-10-056-583-98	Sequence 98, App1
36	51	54.8	15	US-10-056-583-25	Sequence 25, App1
37	50	53.8	15	US-10-056-583-26	Sequence 26, App1
38	50	53.8	15	US-10-056-583-62	Sequence 62, App1
39	50	53.8	15	US-10-094-749-3117	Sequence 3117, App1
40	50	53.8	16	US-10-408-765A-2514	Sequence 2514, App1
41	50	53.8	15	US-10-056-583-29	Sequence 29, App1
42	49	52.7	15	US-10-056-583-44	Sequence 44, App1
43	49	52.7	15	US-09-765-101-19	Sequence 19, App1
44	48	51.6	15	US-09-765-644A-19	Sequence 19, App1
45	48	51.6	15	US-09-765-644A-19	Sequence 19, App1

ALIGNMENTS

RESULT 1

US-10-056-583-89

Sequence 89, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Ströminger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DENEUTLINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

PRIOR FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-89

Query Match 100.0%; Score 93, DB 14, Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKXKYEAAYKAAAAAPA 19
Db 1 APEKXKYEAAYKAAAAAPA 19

RESULT 2
US-10-056-583-88

```
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match      88.2%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APEKAYEAYKAAAAA 17
DB      1 APEKAYEAYKAAAAA 17

RESULT 3
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match      88.2%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 EKAKYEAYKAAAAA 19
DB      1 EKAKYEAYKAAAAA 17

RESULT 4
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match      78.5%; Score 73; DB 14; Length 17;
Best Local Similarity 88.2%; Pred. No. 0.00016;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 APEKAYEAYKAAAAA 17
DB      1 APEKAYEAYKAAAAA 17

RESULT 5
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match      76.3%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 EKAKYEAYKAAAAA 17
DB      1 EKAKYEAYKAAAAA 15

RESULT 6
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
```

```
Query Match          74.2%; Score 69; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00065;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAKAYEAYKAAAAA 17
| | | | | | | | | | |
Db      1 APEKAKFEAFKAAAAA 17
```

```
RESULT 7
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maisha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match          69.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 EAKAYEAYKAAAAA 17
| | | | | | | | | | |
Db      1 EAAKYEAYKAAAAA 15
```

```
RESULT 8
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maisha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95
```

```
Query Match          67.7%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0048;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 EAKAYEAYKAAAAA 17
| | | | | | | | | | |
Db      1 EAKAFKFAKAAAAA 15
```

```
RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maisha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92
```

```
Query Match          66.7%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0069;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 EAKAYEAYKAAAAA 17
| | | | | | | | | | |
Db      1 EAKKEAYKAAAAA 15
```

```
RESULT 10
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maisha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match 65.6%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0098;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
DB 1 EKAKEAYKAAAAA 15

RESULT 11

US-10-056-583-85
Sequence 85, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ. ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 85
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match 65.6%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0098;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
DB 1 EKAKEAYKAAAAA 15

RESULT 12
US-10-056-583-66
Sequence 66, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ. ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 64.5%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.014;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
DB 1 EKAKEAYKAAAAA 15

RESULT 13

US-10-056-583-51
Sequence 51, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ. ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Query Match 63.4%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
DB 1 EKAKEAYKAAAAA 15

RESULT 14
US-10-056-583-53
Sequence 53, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ. ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53

Query Match 63.4%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAAA 17
DB 1 EKAKEAYKAAAAA 15

RESULT 15

US-10-056-583-91
 ; Sequence 91, Application US/10056583
 ; Publication No. US20030064915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presidents and Fellows of Harvard College
 ; APPLICANT: Strominger, Jack L.
 ; APPLICANT: Fridkis-Hareli, Masha
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMENTIATING
 ; FILE OF INVENTION: CONDITIONS
 ; FILE REFERENCE: 24655-017
 ; CURRENT APPLICATION NUMBER: US/10/056,583
 ; CURRENT FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/263,569
 ; PRIOR FILING DATE: 2001-01-24
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 91
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: The peptide was designed and synthesized.
 US-10-056-583-91

Query Match 61.3%; Score 57; DB 14; Length 15;
 Best Local Similarity 80.0%; Pred. No. 0.041;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
 Db 1 EKAKYEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:23
 Job time : 68.8571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 : Search time 16.8673 Seconds
(without alignments)
108.382 Million cell updates/sec

Title: US-10-056-583A-89

Sequence: 1 APEKAYEAYKAAAAA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR:79:*
2: PIR:1:*
3: PIR:3:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	58.1	441	2 A43555	GAP-43-related pro
2	49	52.7	641	2 PH1919	FL-160-4 protein -
3	48	51.6	129	1 TNLJG3	trans-activating t
4	47	50.5	106	1 TNLJG2	trans-activating t
5	47	50.5	108	2 F97521	VC033 protein homo
6	47	50.5	108	2 AH2740	conserved hypochet
7	47	50.5	599	1 QRMSE	estrogen receptor
8	46	49.5	179	2 F97683	50S ribosomal prot
9	46	49.5	339	2 AF2908	chitinase (EC 3.2.
10	46	49.5	339	2 S39979	chitinase (EC 3.2.
11	46	49.5	340	2 S40414	chitinase (EC 3.2.
12	45	48.4	84	2 T23177	hypothetical prote
13	45	48.4	107	2 AB3271	hypothetical prote
14	45	48.4	154	2 H81076	conserved hypochet
15	45	48.4	154	2 B81866	conserved hypochet
16	45	48.4	188	2 I50145	homeotic protein H
17	45	48.4	289	2 A43562	homeotic protein H
18	45	48.4	329	2 D96030	hypothetical prote
19	45	48.4	347	2 A81794	probable rocamase
20	45	48.4	347	2 B81216	peptidyl-prolyl ci
21	45	48.4	447	2 AB3359	dihydrolipoamide S
22	45	48.4	595	2 I47140	estradiol receptor
23	44.5	47.8	189	2 S77930	exoskeletal protei
24	44.5	47.8	189	2 S77935	exoskeletal protei
25	44.5	47.8	600	1 QRRTE	estrogen receptor
26	44	47.3	168	2 T34804	hypothetical prote
27	44	47.3	270	2 T31225	traf protein homol
28	44	47.3	282	2 T51013	related to calmodu
29	44	47.3	398	2 T21061	hypothetical prote

30	44	47.3	421	2 JV0057	tolA protein - Esc
31	44	47.3	503	1 VMU71B	variant surface gl
32	44	47.3	751	1 D72338	(p)pgpp synthetas
33	44	46.8	132	1 MOCHLA	myosin alkali ligh
34	43.5	46.2	49	2 PX0029	protein C inhibito
35	43	46.2	136	2 A10026	50S ribosomal prot
36	43	46.2	162	2 H70927	probable rpa prot
37	43	46.2	176	2 G87606	transcription regu
38	43	46.2	185	2 S36290	T-cell receptor ga
39	43	46.2	379	2 T08277	carotenoid biosynt
40	43	46.2	436	2 I51237	translation elonga
41	43	46.2	436	2 S20060	translation elonga
42	42	46.2	736	2 D96830	probable heat-shoc
43	42	45.2	109	2 T02039	acidic ribosomal p
44	42	45.2	109	2 T02716	acidic ribosomal p
45	42	45.2	136	1 R5EC16	ribosomal protein

ALIGNMENTS

RESULT 1
A43555
GAP-43-related protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: A43555; S65398
R:Ng, S.C.; Perkins, L.A.; Conboy, G.; Perrimon, N.; Fishman, M.C.
Development 105, 629-638, 1989
A>Title: A Drosophila gene expressed in the embryonic CNS shares one conserved domain w
A/Reference number: A43555; MUID:90126372; PMID:2693037
A/Accession: A43555
A/Molecule type: mRNA
A/Residues: 1-441 <NGA>
A/Cross-references: UNIPROT: P29746; EMBL: X63828
R:Perkins, L.A.
submitted to the EMBL Data Library, December 1991
A/Reference number: S65398
A/Accession: S65398
A/Molecule type: mRNA
A/Residues: 1-111, 'AIPKKTU', '120', 'EBAK', '125', 'A0ENM', '131', 'VEAKKQKQKARTRE', '146', 'EPTVEAP'
A/Cross-references: EMBL: X63828; NID: 97663; PID: 97664
C/Note: the differences in residues 112-178 are due to frameshift errors
C/Genetics:
A/Gene: FLYBase: dnb
A/Cross-references: FLYBase: F8gn0001090
A/Map position: 10

Query Match 58.1%; Score 54; DB 2; Length 441;
Best Local Similarity 63.2%; Pred. No. 1.6;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Dy 1 APEKAYEAYKAAAAA 19
Db 263 APEKAYEAYKAAAAA 281

RESULT 2
PH1919
FL-160-4 protein - Trypanosoma cruzi (fragment)
C:Species: Trypanosoma cruzi
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: PH1919; S32017
R:Van Voorthuis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.
J. Exp. Med. 178, 681-694, 1993
A>Title: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene family and
A/Reference number: JH0823; MUID:93340646; PMID:7688032
A/Accession: PH1919
A/Molecule type: DNA
A/Residues: 1-641 <VAN>
A/Cross-references: UNIPROT: Q05508
R:Van Voorthuis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.
submitted to the EMBL Data Library, February 1993

A>Description: Ft-160 proteins of Trypanosoma cruzi are expressed from a multigene family
A:Reference number: S32015
A:Accession: S32017

A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-289, 'L', 291-309, 'N', 311-641 <VA2>

A:Cross-references: EMBL:X70950; NID:g11162; PID:g11163

C:Keywords: glycoprotein
F:115,130,224,575,590/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.7%; Score 49; DB 2; Length 641;
Best Local Similarity 47.4%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAAPA 19

DB 376 SPEKSKYKEXYKAGSAGAP 394

RESULT 3

TNLU3
trans-activating transcription regulator - simian immunodeficiency virus (macaque isolat

C:Species: simian immunodeficiency virus, SiV

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: F28887

R:Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.

Nature 328, 543-547, 1987

A>Title: Sequence of simian immunodeficiency virus from macaque and its relationship to

A:Reference number: A28887; MUID:87287230; PMID:3649576

A:Accession: F28887

A:Molecule type: DNA

A:Residues: 1-129 <CHA>

A:Cross-references: UNIPROT:P05911; GB:Y00277; GB:M16403; NID:961730

A:Gene: tat

C:Genetics:

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription

Query Match 51.6%; Score 48; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 4;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAYEAYKAAAAAPA 18

DB 109 PKAKKETVEAAVATAP 125

RESULT 4

TNLU32
trans-activating transcription regulator - simian immunodeficiency virus SiVagm (type 3,

C:Species: simian immunodeficiency virus SiVagm

C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: A26737

R:Hirsch, V.; Riedel, N.; Mullins, J.I.

Cell 49, 307-319, 1987

A>Title: The genome organization of SiV-3 is similar to that of the AIDS virus except f

A:Reference number: A26737; MUID:87187627; PMID:3646094

A:Accession: A26737

A:Molecule type: DNA

A:Residues: 1-106 <HIR>

A:Cross-references: UNIPROT:P11263; GB:M19499; NID:g334657

A>Note: the authors translated the codon GAC for residue 9 as Asn

C:Genetics:

A:Gene: tat

A:Insertions: 74/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; transcription

Query Match 50.5%; Score 47; DB 1; Length 106;
Best Local Similarity 58.8%; Pred. No. 4.7;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAYEAYKAAAAAPA 18

DB 86 PEKAKKETVEAAVATAP 102

RESULT 5

F97521
VCO33 protein homolog (AF179595) [imported] - Agrobacterium tumefaciens (strain C58, Cel

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: F97521

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; McIlm, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.,

Science 294, 2323-2328, 2001

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: F97521

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <KUR>

A:Cross-references: UNIPROT:Q8UFR1; GB:AE007869; PIDN:AAK87127.1; PID:g15156391; GSPDB:

C:Genetics: AGR_C 2462

A:Map position: circular chromosome

Query Match 50.5%; Score 47; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4.8;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAAPA 19

DB 60 AAYEAYRRLAADPA 74

RESULT 6

AH2740
conserved hypothetical protein Atu1336 [imported] - Agrobacterium tumefaciens (strain C5

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AH2740

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AH2740

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <KUR>

A:Cross-references: UNIPROT:Q8UFR1; GB:AE008668; PIDN:AAI42342.1; PID:g17739747; GSPDB:

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu1336

A:Map position: circular chromosome

Query Match 50.5%; Score 47; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4.8;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAAPA 19

DB 60 AAYEAYRRLAADPA 74

RESULT 7

QKMS

estrogen receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: A40061

R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
A;Accession: A40061
A;Molecule type: mRNA
A;Residues: 1-599 <WHI>
A;Cross-references: UNIPROT:P19785; GB:M38651; NID:G193179; PIDN:AAA37580.1; PID:G193180
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-183/Domain: amino-terminal <NR2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-460/Domain: erba transforming protein homology <ERBA>
F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <SRB>
F;189.192.206.209/Binding site: zinc (Cys) #status predicted
F;225.231.241.244/Binding site: zinc (Cys) #status predicted
F;240.309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 50.5%; Score 47; DB 1; Length 599;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 PERAKYEAAYKAAAPAA 19
|||:|||||
Db 55 PEGAAVEFNMAAAAAA 72

RESULT 8
F;97683
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97683
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:117433194
A;Accession: F97683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK68423.1; PID:G15157917; GSPDB:C
C;Genetics:
A;Gene: AGR_C_4900
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 49.5%; Score 46; DB 2; Length 179;
Best Local Similarity 63.2%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAXYEAAYKAAAPAA 19
|||:|||||
Db 135 ABEKARLEAEKVAAQAALA 153

RESULT 9
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2908
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AA43684.1; PID:G17741210; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rplS
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 49.5%; Score 46; DB 2; Length 179;
Best Local Similarity 63.2%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAXYEAAYKAAAPAA 19
|||:|||||
Db 135 ABEKARLEAEKVAAQAALA 153

RESULT 10
S39979
chitinase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S39979
R;Nishizawa, Y.; Kishimoto, N.; Salto, A.; Hibl, T.
Mol. Gen. Genet. 241, 1-10, 1993
A;Title: Sequence variation, differential expression and chromosomal location of rice c
A;Reference number: S39979; MUID:94049667; PMID:7901749
A;Accession: S39979
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-339 <NIS>
A;Cross-references: UNIPROT:Q43294; EMBL:X56787
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;33-74/Domain: hevein chitin-binding domain homology <HCB>
F;91-329/Domain: plant chitinase homology <PCH>

Query Match 49.5%; Score 46; DB 2; Length 339;
Best Local Similarity 76.9%; Pred. No. 20;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 YEAYKAAAPAA 19
|||:|||||
Db 117 YEAFMAAAAPAA 129

RESULT 11
S40414
chitinase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S40414
R;Nishizawa, Y.
submitted to the EMBL Data Library, November 1990
A;Reference number: S40414
A;Accession: S40414
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-340 <NIS>
A;Cross-references: UNIPROT:Q43294; EMBL:X56787; NID:G407471; PIDN:CAA40107.1; PID:G407
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;33-74/Domain: hevein chitin-binding domain homology <HCB>
F;92-330/Domain: plant chitinase homology <PCH>

Query Match 49.5%; Score 46; DB 2; Length 340;

Best Local Similarity 76.9%; Pred. No. 20;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YENYKAAAAAPA 19
DB 118 YEAFLAAAAAPA 130

RESULT 12

T23177
hypothetical protein K01D12.7 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T23177; T23188
R/Dobson, R.

submitted to the EMBL Data Library, June 1996

A/Reference number: Z19703

A/Accession: T23177
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-84 <W12>

A/Cross-references: UNIPROT:Q27223; UNIPROT:Q95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB:

A/Experimental source: clone K01D12

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-84 <W12>

A/Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CBSP:K01D12.15

A/Experimental source: clone K01D12

C/Genetics:
A/Map position: 5

Query Match 48.4%; Score 45; DB 2; Length 84;
Best Local Similarity 61.1%; Pred. No. 7.5;

Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 PEKAKYEAAYKAAAAA 19
DB 34 PPKASATKAAAPAA 51

RESULT 13

AB3271
hypothetical protein BME10151 [imported] - *Brucella melitensis* (strain 16M)

C/Species: *Brucella melitensis*
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C/Accession: AB3271
R/DelVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A/Reference number: AD3252; PMID:11756688

A/Accession: AB3271
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-107 <KUD>

A/Cross-references: UNIPROT:O8YD5; GB:AE008917; PIDN:AAL5133.1; PID:G17982031; GSPDB:

A/Experimental source: strain 16M

C/Genetics:
A/Map position: 1

Query Match 48.4%; Score 45; DB 2; Length 107;
Best Local Similarity 52.9%; Pred. No. 9.5;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKYEAAYKAAAAA 18
DB 57 PSLADYEAYRSLAADP 73

RESULT 14

H81076
conserved hypothetical protein NMB1500 [imported] - *Neisseria meningitidis* (strain MC58)

C/Species: *Neisseria meningitidis*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: H81076
R/Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamadevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizzia, M.

Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Vc

A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A/Reference number: AB1000; MUID:20175755; PMID:10710307

A/Accession: H81076
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-154 <TET>

A/Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:97226737; PIDN:AAF4185

A/Experimental source: serogroup B, strain MC58

C/Genetics:
A/Map position: 5

Query Match 48.4%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 16
DB 48 APEFLQHESEYAAAVA 63

RESULT 15

B81866
conserved hypothetical protein NMA1703 [imported] - *Neisseria meningitidis* (strain Z2491)

C/Species: *Neisseria meningitidis*
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: B81866
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagers, K.; Leather, S.; Moulle, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A/Reference number: AB1775; MUID:20222556; PMID:10761919

A/Accession: B81866
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-154 <PAR>

A/Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB8493

A/Experimental source: serogroup A, strain Z2491

C/Genetics:
A/Map position: 3

Query Match 48.4%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 16
DB 48 APEFLQHESEYAAAVA 63

Search completed: February 26, 2005, 23:57:15
Job time : 17.8673 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 82.5918 Seconds

(without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583A-89

Perfect score: 93

Sequence: 1 APEKAKYEAYKAAAAAPA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.1	319	2	Q9N603	Q9n603 drosophila
2	54	319	2	Q9N603	Q9n603 drosophila
3	54	319	2	Q9N603	Q9n603 drosophila
4	54	319	2	Q9N603	Q9n603 drosophila
5	54	319	2	Q9N603	Q9n603 drosophila
6	54	319	2	Q9N603	Q9n603 drosophila
7	54	319	2	Q9N603	Q9n603 drosophila
8	54	319	2	Q9N603	Q9n603 drosophila
9	54	319	2	Q9N603	Q9n603 drosophila
10	54	319	2	Q9N603	Q9n603 drosophila
11	54	319	2	Q9N603	Q9n603 drosophila
12	54	319	2	Q9N603	Q9n603 drosophila
13	54	319	2	Q9N603	Q9n603 drosophila
14	54	319	2	Q9N603	Q9n603 drosophila
15	54	319	2	Q9N603	Q9n603 drosophila
16	54	319	2	Q9N603	Q9n603 drosophila
17	54	319	2	Q9N603	Q9n603 drosophila
18	54	319	2	Q9N603	Q9n603 drosophila
19	54	319	2	Q9N603	Q9n603 drosophila
20	54	319	2	Q9N603	Q9n603 drosophila
21	54	319	2	Q9N603	Q9n603 drosophila
22	54	319	2	Q9N603	Q9n603 drosophila
23	54	319	2	Q9N603	Q9n603 drosophila
24	54	319	2	Q9N603	Q9n603 drosophila
25	54	319	2	Q9N603	Q9n603 drosophila
26	54	319	2	Q9N603	Q9n603 drosophila
27	54	319	2	Q9N603	Q9n603 drosophila
28	54	319	2	Q9N603	Q9n603 drosophila
29	54	319	2	Q9N603	Q9n603 drosophila
30	54	319	2	Q9N603	Q9n603 drosophila
31	54	319	2	Q9N603	Q9n603 drosophila

32	47	50.5	315	2	Q9N603	Q9n603 drosophila
33	47	50.5	375	2	Q9N603	Q9n603 drosophila
34	47	50.5	409	2	Q9N603	Q9n603 drosophila
35	47	50.5	409	2	Q9N603	Q9n603 drosophila
36	47	50.5	599	1	ESR1_MOUSE	Q9d6f6 xenopus lae
37	47	50.5	599	1	ESR1_MOUSE	Q9d6f6 xenopus lae
38	47	50.5	616	2	Q9LD96	P19785 mus musculu
39	47	50.5	753	2	Q9LD96	Q9ld96 oryza sativ
40	47	50.5	753	2	Q9LD96	Q9ld96 burkholderi
41	46.5	50.0	111	2	Q6MAY0	Q6m3g0 burkholderi
42	46.5	50.0	300	2	Q729M4	Q6m3g0 burkholderi
43	46	49.5	179	1	RL19_AGR75	Q729m4 desulfovibr
44	46	49.5	196	2	Q8KLA9	Q8k1a9 agrobacteri
45	46	49.5	200	2	P82166	Q8k1a9 rhizobium e
					H1_NEUCR	P82166 locusta mig
						Q9jou2 neurospora

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	319 AA
Q9N603			
AC Q9N603			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Bangles and beads protein (Fragment).			
GN Name=bnb;			
OS Drosophila simulans (Fruit fly).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC Ephydroidea; Drosophilidae; Drosophila.			
OX NCBI_TaxID=7240;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Sim5, Sim2, and Sim3;			
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;			
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).			
DR EMBL; AF256066; AAF68652.1; -			
DR EMBL; AF256066; AAF68652.1; -			
DR EMBL; AF256067; AAF68653.1; -			
DR FlyBase; FBgn0041666; Dsim\bnb.			
FT NON_TER			
FT SEQUENCE 319 AA; 33129 MW; FEFBSA8D601C2B67 CRC64;			
Query Match	58.1%	Score 54; DB 2; Length 319;	
Best Local Similarity	63.2%	Pred. No. 6.9;	
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY 1 APEKAKYEAYKAAAAAPA 19			
DB 141 APEKAKYEAYKAAAAAPA 159			
RESULT 2			
Q9N603			
ID Q9N603	PRELIMINARY;	PRT;	319 AA.
AC Q9N603			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE Bangles and beads protein (Fragment).			
GN Name=bnb;			
OS Drosophila simulans (Fruit fly).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC Ephydroidea; Drosophilidae; Drosophila.			
OX NCBI_TaxID=7240;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Sim8;			

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RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256072; AAF68658.1; -.
DR FlyBase; FBgn0041666; Ds1m\hnb.
FT NON TER
SQ SEQUENCE 319 AA; 33169 MW; 0536BA5182AACA7 CRC64;

QY
Db 1 APEKAYEAYKAAAAAPA 19
141 APEKKSIESPPAAAAAPA 159

Query Match 58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 3
QNG87 PRELIMINARY; PRT; 319 AA.
AC QNG87;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=hnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim7;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256071; AAF68657.1; -.
DR FlyBase; FBgn0041666; Ds1m\hnb.
FT NON TER
SQ SEQUENCE 319 AA; 33185 MW; B1178655BESD662D CRC64;

Query Match 58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY
Db 1 APEKAYEAYKAAAAAPA 19
141 APEKKSIESPPAAAAAPA 159

RESULT 4
QNG88 PRELIMINARY; PRT; 319 AA.
AC QNG88;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=hnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim6;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";

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RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256070; AAF68656.1; -.
DR FlyBase; FBgn0041666; Ds1m\hnb.
FT NON TER
SQ SEQUENCE 319 AA; 33165 MW; FC7EF5A566FDP92D CRC64;

QY
Db 1 APEKAYEAYKAAAAAPA 19
141 APEKKSIESPPAAAAAPA 159

Query Match 58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 5
QNG89 PRELIMINARY; PRT; 319 AA.
AC QNG89;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=hnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim4;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256068; AAF68654.1; -.
DR FlyBase; FBgn0041666; Ds1m\hnb.
FT NON TER
SQ SEQUENCE 319 AA; 33157 MW; A2020D5038CE7625 CRC64;

Query Match 58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY
Db 1 APEKAYEAYKAAAAAPA 19
141 APEKKSIESPPAAAAAPA 159

RESULT 6
QNG90 PRELIMINARY; PRT; 319 AA.
AC QNG90;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=hnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim1;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256065; AAF68651.1; -.
DR FlyBase; FBgn0041666; Ds1m\hnb.

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FT NON TER 1 1
SQ SEQUENCE 319 AA; 33157 MW; EDEED188E68F3B6F CRC64;
Query Match 58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
1 APEKXKYEAYKAAAAAPA 19
141 APEKXKYEAYKAAAAAPA 159
Db 141 APEKXKYEAYKAAAAAPA 159
RESULT 7
BNB_DROME STANDARD; PRT; 442 AA.
AC P29746; Q9VW00;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Bangles and beads protein.
GN Name=bnb; ORFNames=CG7088;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Hymenoptera; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90126372; PubMed=2693037;
RA Ng S.C., Perkins L.A., Conboy G., Perrimon N., Fishman M.C.;
RT "A Drosophila gene expressed in the embryonic CNS shares one conserved
RL domain with the mammalian GAP-43.";
RU Development 105:629-638(1989).
RN [2]
RP REVISIONS.
RX MEDLINE=92201643; PubMed=1551578;
RA Beiri D.F., Perkins L.A., Engelstein M., Hilliker A.J., Perrimon N.;
RT "Genetic and developmental analysis of polytene section 17 of the X
RL chromosome of Drosophila melanogaster.";
RU Genetics 130:569-583(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
RA Beeson K.Y., Beron P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davis P.,
RA de Paolis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.O., Hernandez J.R., Houck J.,
RA Heston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny L., Nelson D.L.,
RA Nelson D.M., Nelson K.A., Nixon K., Nusekern D.R., Paclob J.M.,
RA Palazzolo M., Plutman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RU Science 287:2185-2195(2000).
RL [4]
RN [4]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Paclob J.M., Park S., Wan K.H.,
RA Rubin G.M., Celisner S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -1- FUNCTION: May play an important role during development.
CC -1- TISSUE SPECIFICITY: Expressed in the embryonic CNS, in sets of
CC cells that are segmentally reiterated along the periphery of the
CC nervous system.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X63828; CAA45323.1; -;
DR EMBL; AE003510; AAF48888.1; -;
DR EMBL; AY060682; AAL28230.1; -;
DR PIR; A43555; A43555;
DR FlyBase; FBgn0010950; bnb.
DR GO; GO:0007275; P:development; IMP.
DR GO; GO:0042063; P:glutogenesis; IEP.
KW Developmental protein.
SQ SEQUENCE 442 AA; 45815 MW; 8EB67F77656A1200 CRC64;
Query Match 58.1%; Score 54; DB 1; Length 442;
Best Local Similarity 63.2%; Pred. No. 9.4;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
1 APEKXKYEAYKAAAAAPA 19
264 APEKXKYEAYKAAAAAPA 282
Db 264 APEKXKYEAYKAAAAAPA 282
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AC 096M46;
DT 01-DEC-2001 (TRIMBLrel. 19, Created)
DT 01-DEC-2001 (TRIMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ32830.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,
 Sekine W., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
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 Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
 Kanehori K., Takahashi-Fujii A., Hara R., Tanase T., Nomura Y.,
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 Yoshioka K., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
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 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujimura T.,
 Oono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Okamoto S.,
 Kawabata A., Hiki K., Kobayashi N., Inagaki H., Ikema Y., Okamoto S.,
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 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 Taniguchi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maehira Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai S., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL: AK057392; BAB71466.1; -
 DR InterPro: IPR008938; ARM.
 SQ SEQUENCE 570 AA; 65769 MW; 65BEB6F244FCE2 CRC64;

Query Match 53.8%; Score 50; DB 2; Length 570;
 Best Local Similarity 69.2%; Pred. No. 47;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAA 14
 ID Q7S628 PRELIMINARY; PRT; 993 AA.
 AC Q7S628;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU05565.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
 Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 Qui D., Iankov P., Pedersen D., Nelson M., Washburne M.,
 Seltzer M., Kistner J., Brahm J., Brown E.L., Zeller A., Schulte U.,
 Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnanapavan S.,

RA Kamal M., Kamysellie M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 Kryazov S., Rasmussen C., Metzner R.L., Perkins D.D., Kroken S.,
 Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmati S.A.,
 Desouza C.C., Glaes U., Orbach M.J., Berglund J., Voelker R.,
 Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 Natvig D.O., Alex L.A., Manhaupt G., Ebbola D.J., Freitag M.,
 Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RT Nature 0:0-0(2003).
 RL Nature 0:0-0(2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL: AABX01000321; EAA31291.1; -
 DR EMBL: AABX01000321; EAA31291.1; -
 SQ SEQUENCE 993 AA; 107526 MW; 4A954861D16D763F CRC64;

Query Match 53.8%; Score 50; DB 2; Length 993;
 Best Local Similarity 66.7%; Pred. No. 80;
 Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAP 18
 ID Q05508 PRELIMINARY; PRT; 641 AA.
 AC Q05508;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Flagellum-Associated Protein (Fragment).
 GN Name=FL-160-4;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 NCBI_TaxID=5693;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL;
 RX MEDLINE=93340646; PubMed=7688032;
 RA Van Voorthuis W.C., Barrett L., Koelling R., Farr A.G.;
 RT "FL-160 proteins of Trypanosoma cruzi are expressed from a multigene
 family and contain two distinct epitopes that mimic nervous tissues.";
 RL J. Exp. Med. 178:681-694(1993).
 DR EMBL: X70950; CAA50289.1; -
 DR PIR: PH1919; PH1919.
 DR HSSP: O44049; INIT.
 DR GO: GO:0004308; F:exo-alpha-sialidase activity; IEA.
 DR GO: GO:0009405; P:patogenesis; IEA.
 DR InterPro: IPR008985; ConA-like lec.gl.
 DR InterPro: IPR008377; Sialidase-trypan.
 DR PRINTS: PR01803; TCSIALIDASE.
 FT NON_TER 1
 SQ SEQUENCE 641 AA; 68938 MW; 36C9928C010D5F4B CRC64;

Query Match 52.7%; Score 49; DB 2; Length 641;
 Best Local Similarity 47.4%; Pred. No. 75;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAPA 19
 ID Q05508 PRELIMINARY; PRT; 130 AA.
 AC Q05508;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE TAT protein (Transactivating regulatory protein).
 GN Name=TAT;

OS Simian immunodeficiency virus (Mm142-83 isolate) (SIV-MAC).
 CC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 CX NCBI_TaxID=11733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87287230; PubMed=3649576; DOI=10.1038/328543a0;
 RA Chakrabarti L., Guyader M., Alizon M., Daniel M.D., Desrochers R.C.,
 RA Tiollais P., Sonigo P.;
 RT "Sequence of simian immunodeficiency virus from macaque and its
 RT relationship to other human and simian retroviruses";
 RL Nature 328:543-547(1987).
 CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
 CC trans-activating responsive sequence (TAR) RNA element and
 CC activates transcription initiation and/or elongation from the LTR
 CC promoter.
 CC -1- SUBUNIT: Binds cyclin T1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -1- MISCELLANEOUS: This is a macaque isolate.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y00277; CAB46521.1; -;
 DR F1R; F28887; TNLJG3.
 DR HSP; P12506; ITBC.
 DR HIV; M16403; TATSM142.
 DR InterPro: IPR001831; IV_Tat.
 DR Pfam: PF00539; Tat.1.
 DR PRINTS; PR00055; HIVTATDOMA1N.
 DR Activator; AIDS; Nuclear protein; RNA-binding;
 KW Transcription regulation.
 SQ SEQUENCE 130 AA; 14545 MW; DA133BCABAF7F521 CRC64;

Query Match 51.6%; Score 48; DB:1; Length 130;
 Best Local Similarity 58.8%; Pred. No. 23;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PEKAYEAYKAAAP 18
 Db 110 PKAKKETVBAVATAP 126

RESULT 12
 Q9VFL4 PRELIMINARY; PRT; 300 AA.
 ID Q9VFL4; PRELIMINARY; PRT; 300 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 18, Last annotation update)
 DE CG14840-PA (AT18408p).
 GN ORFNames=CG14840;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazee R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter C., Heit G., Nelson C.R., Gaber G.L.,
 RA Arlitt J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brooksstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport U.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry B., Murthy L., Muzny D.M., Nelson D.L.,
 RA Mount S.M., Moy M., Murphy B., Murthy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537566;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [7]
 RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarino H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AE003704; AAF55038.1; -;
 DR EMBL: AY089356; AAL90094.1; -;
 DR Inact; Q9V7U6; -;
 DR FLYBase: FBgn0038217; CG14840.
 DR InterPro: IPR007999; DUF745.
 DR Pfam: PF05335; DUF745; 1.
 SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;

Query Match 51.6%; Score 48; DB 2; Length 300;
 Best Local Similarity 64.7%; Pred. No. 52;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 EXAKTEAYKAAAPAA 19
 DB 242 EKTQAAAYKAACAAVEA 258

RESULT 13
 ID Q9V7U6 PRELIMINARY; PRT; 463 AA.
 AC Q9V7U6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE CG6301-PA.
 GN ORNames=CG6301;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neuroptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalaia M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Stapleton M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasmann D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 Science 287:2185-2195 (2000).
 RL
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RT Genome Biol. 3:RESEARCh0079-RESEARCh0079 (2002).
 RL
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective."
 RT Genome Biol. 3:RESEARCh0084-RESEARCh0084 (2002).
 RL
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupry J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RT Genome Biol. 3:RESEARCh0083-RESEARCh0083 (2002).
 RL
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003805; AAF57947.2; -;
 DR Inact; Q9V7U6; -;
 DR FLYBase: FBgn0034161; CG6301.
 DR InterPro: IPR007999; DUF745.
 DR Pfam: PF05335; DUF745; 1.
 SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEF6BEC9 CRC64;

Query Match 51.6%; Score 48; DB 2; Length 463;
 Best Local Similarity 64.7%; Pred. No. 78;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 EXAKTEAYKAAAPAA 19
 DB 275 EKTQAAAYKAACAAVEA 291

RESULT 14
 ID Q64CP3 PRELIMINARY; PRT; 707 AA.
 AC Q64CP3;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORNames=G21D1_21;

OS uncultured archaeon GZfosid1.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=286721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15353801;
 RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
 RT "Reverse mechanogenesis: testing the hypothesis with environmental
 RT genomics.";
 RL Science 305:1457-1462(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY114833; AAU82834.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match 51.6%; Score 48; DB 2; Length 707;
 Best Local Similarity 70.6%; Pred. No. 1.2e+02;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAAAA 17
 |||||
 Db 643 AAEKXSEARAAAAA 659

RESULT 15

Q82KI6 PRELIMINARY; PRT; 949 AA.
 ID O82KI6;
 AC O82KI6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderelocusNames=SAV2417;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005030; BAC70128.1; -.
 DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
 DR InterPro; IPR003781; COA_binding.
 DR InterPro; IPR000182; GCN5acetyl_trans.
 DR Pfam; PF00583; Acetyltransf_1; 1.
 DR Pfam; PF02629; COA_binding_1;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 949 AA; 100557 MW; 98B8E5ED93FC9D3 CRC64;

Query Match 51.6%; Score 48; DB 2; Length 949;
 Best Local Similarity 57.9%; Pred. No. 1.5e+02;
 Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAAAA 19
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 Db 582 AADQALAEALRSAAAAA 600

Search completed: February 26, 2005, 23:55:41
 Job time : 84.5918 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 86.9082 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583A-90

Perfect score: 82

Sequence: 1 EKAKYKAKAAAAA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	17	5	ABP52296 HLA-DR2 m
2	82	100.0	19	5	ABP52295 HLA-DR2 m
3	71	86.6	15	5	ABP52271 HLA-DR2 m
4	71	86.6	15	5	ABP52298 HLA-DR2 m
5	71	86.6	17	5	ABP52294 HLA-DR2 m
6	65	79.3	15	5	ABP52270 HLA-DR2 m
7	63	76.8	15	5	ABP52301 HLA-DR2 m
8	62	75.6	17	5	ABP52303 HLA-DR2 m
9	61	74.4	15	5	ABP52291 HLA-DR2 m
10	61	74.4	15	5	ABP52263 HLA-DR2 m
11	60	73.2	15	5	ABP52272 HLA-DR2 m
12	59	72.0	15	5	ABP52259 HLA-DR2 m
13	59	72.0	15	5	ABP52257 HLA-DR2 m
14	58	70.7	17	5	ABP52302 HLA-DR2 m
15	57	69.5	15	5	ABP52297 HLA-DR2 m
16	56	68.3	15	5	ABP52253 HLA-DR2 m
17	56	68.3	15	5	ABP52251 HLA-DR2 m
18	56	68.3	15	5	ABP52239 HLA-DR2 m
19	55	67.1	15	5	ABP52290 HLA-DR2 m
20	55	67.1	15	5	ABP52261 HLA-DR2 m
21	55	67.1	15	5	ABP52244 HLA-DR2 m
22	55	67.1	15	5	ABP52292 HLA-DR2 m
23	55	67.1	15	5	ABP52269 HLA-DR2 m
24	55	67.1	15	5	ABP52262 HLA-DR2 m
25	54	65.9	15	5	ABP52264 HLA-DR2 m

26	54	65.9	15	5	ABP52267 HLA-DR2 m
27	54	65.9	15	5	ABP52236 HLA-DR2 m
28	53	64.6	15	5	ABP52299 HLA-DR2 m
29	52	63.4	15	5	ABP52265 HLA-DR2 m
30	51	62.2	15	5	ABP52254 HLA-DR2 m
31	51	62.2	15	5	ABP52255 HLA-DR2 m
32	51	62.2	15	5	ABP52240 HLA-DR2 m
33	51	62.2	15	5	ABP52241 HLA-DR2 m
34	51	62.2	15	5	ABP52304 HLA-DR2 m
35	51	62.2	15	5	ABP52248 HLA-DR2 m
36	51	62.2	15	5	ABP52249 HLA-DR2 m
37	50	61.0	15	5	ABP52232 HLA-DR2 m
38	50	61.0	15	5	ABP52268 HLA-DR2 m
39	50	61.0	15	5	ABP52231 HLA-DR2 m
40	49	59.8	15	5	ABP52235 HLA-DR2 m
41	49	59.8	15	5	ABP52250 HLA-DR2 m
42	48	58.5	15	3	AAV58982 Copeptide
43	48	58.5	15	3	AAV82074 MHC class
44	48	58.5	15	4	AAV63193 Peptide w
45	48	58.5	15	5	ABP52277 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52296 standard; peptide; 17 AA.
ID ABP52296 standard; peptide; 17 AA.
AC ABP52296;
XX
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
PI WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
CC
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 82; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAPAA 17
DB 1 EKAKYEAYKAAAPAA 17
RESULT 2
ABP52295
ID ABP52295 standard; peptide; 19 AA.
XX
AC ABP52295;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200259143-A2.
FN
XX 01-AUG-2002.
PD
XX 24-JAN-2002; 2002WO-US002071.
PF
XX 24-JAN-2001; 2001US-0263569P.
PR
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 19 AA;
Query Match 100.0%; Score 82; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAPAA 17
DB 3 EKAKYEAYKAAAPAA 19
RESULT 3
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200259143-A2.
PN
XX 01-AUG-2002.
PD
XX 24-JAN-2002; 2002WO-US002071.
PF
XX 24-JAN-2001; 2001US-0263569P.
PR
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
PT
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 86.6%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAPAA 15

Db |||||
1 EKAKYEAYKAAAAA 15

RESULT 4

ABP52298 standard; peptide; 15 AA.

XX ABP52298;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:92.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; anti-inflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 15 AA;

Query Match 86.6%; Score 71; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00014; Mismatches 0; Gaps 0;

Qy 1 EKAKYEAYKAAAAA 15
|||
1 EKAKYEAYKAAAAA 15

RESULT 5
ABP52294 standard; peptide; 17 AA.

XX ABP52294;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:88.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; anti-inflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.

XX Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 17 AA;

Query Match 86.6%; Score 71; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Gaps 0;

Qy 1 EKAKYEAYKAAAAA 15
|||
3 EKAKYEAYKAAAAA 17

RESULT 6

ABP52270 standard; peptide; 15 AA.

XX ABP52270;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:64.

KW		Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM	HNA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;	
KX	immune response; antiinflammatory; neuroprotective; proliferation;	
KV	MHC class II protein inhibitor; demyelinating disease; inhibition;	
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;	
KM	anti-tumour necrosis factor agent.	
XX		
OS	Homo sapiens.	
XS	Synthetic.	
PN	WO200259143-A2.	
PN		
PD	01-AUG-2002.	
PP	24-JAN-2002; 2002MO-USO02071.	
PR	24-JAN-2001; 2001US-0263569P.	
PA	(HARD) HARVARD COLLEGE.	
PI	Strominger JL, Fridkis-Harell M.;	
DY	WPI; 2002-608439/65.	
XK		
PT	New compositions comprising synthetic peptides in complex with a major	
PT	histocompatibility complex class II HLA-D2 protein, useful for treating a	
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral	
PT	encephalomyelitis.	
PS	Claim 28; Page 39; 54pp; English.	
CC	The present invention describes compositions (I) comprising a peptide	
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine	
CC	residues. The complex of the peptide with a major histocompatibility	
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an	
CC	immune response. (II) has antiinflammatory and neuroprotective activities,	
CC	and can be used as a MHC class II protein inhibitor. The compositions	
CC	comprising the peptides are useful for treating demyelinating diseases	
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine	
CC	demyelinating condition, and a side effect of administering an anti-	
CC	tumour necrosis factor agents. The peptide further inhibits proliferation	
CC	of autotransigen-specific HLA-DR2-restricted T cell clones. ABP52207 to	
CC	ABP53305 represent peptides used in the exemplification of the present	
CC	invention	
XX		
SQ	Sequence 15 AA:	
	Query Match 79.3%; Score 65; DB 5; Length 15;	
	Best Local Similarity 93.3%; Pred. No. 0.0013;	
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY		
	1 EKAKEYAYKKAAAAA 15	
DB	1 EAAKYEAYRAAAA 15	
	.	
RESULT 7		
ID	ABP52301	
AC	ABP52301 standard; peptide; 15 AA.	
XX		
AC	ABP52301;	
XX		
DT	16-OCT-2002 (first entry)	
DE		
XX	HLA-DR2 molecule binding peptide SEQ ID NO:95.	
XX		
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;	
KM	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;	
KX	immune response; antiinflammatory; neuroprotective; proliferation;	
KV	MHC class II protein inhibitor; demyelinating disease; inhibition;	
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;	
KM	anti-tumour necrosis factor agent.	
XX		

XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	PD	WO200259143-A2.
XX	PD	01-AUG-2002.
XX	PF	24-JAN-2002; 2002WO-US002071.
XX	PR	24-JAN-2001; 2001US-0263569P.
XX	PA	(HARD) HARVARD COLLEGE.
XX	PI	Strominger JL, Fridkis-Hareli M,
XX	DR	WPI; 2002-608439/65.
XX	PT	New compositions comprising synthetic peptides in complex with a major
XX	PT	histocompatibility complex class II HLA-DQ protein, useful for treating a
XX	PT	demyelinating disease, e.g. multiple sclerosis, or post-viral
XX	PS	encephalomyelitis.
XX	PS	Claim 28; Page 39; 54pp; English.
CC	CC	The present invention describes compositions (I) comprising a peptide
CC	CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	CC	residues. The complex of the peptide with a major histocompatibility
CC	CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	CC	immune response. (II) has antiinflammatory and neuroprotective activities,
CC	CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	CC	comprising the peptides are useful for treating demyelinating diseases
CC	CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	CC	tumour necrosis factor agents. The peptide further inhibits proliferation
CC	CC	of autotransgenic-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC	CC	ABP52305 represent peptides used in the exemplification of the present
CC	CC	invention
XX	XX	Sequence 15 AA;
XX	XX	
XX	XX	Query Match 76.8%; Score 63; DB 5; Length 15;
XX	XX	Best Local Similarity 86.7%; Pred. No. 0.0028;
XX	XX	Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
QY		1 EKAKYEAYKAAAAAA 15
		:
DB		1 EKAKEAFKAAAAAA 15
RESULT 8		
ABP52303		
ID		ABP52303 standard; peptide; 17 AA.
XX		
AC		ABP52303;
XX		
DT		16-OCT-2002 (first entry)
XX		
DE		HLA-DR2 molecule binding peptide SEQ ID NO:97.
XX		
KW		human leukocyte antigen, HLA; major histocompatibility complex; MHC;
KW		HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW		immune response; anti-inflammatory; neuroprotective; proliferation;
KW		MHC class II protein inhibitor; demyelinating disease; inhibition;
KW		post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW		anti-tumour necrosis factor agent.
XX		
OS		Homo sapiens.
OS		Synthetic.
XX		
PN		WO200259143-A2.
XX		
PD		01-AUG-2002.

PE 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 75.6%; Score 62; DB 5; Length 17;
 Best Local Similarity 86.7%; Pred. No. 0.0046;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 EKAKYEAYKAAAAA 15
 |||:|||||
 Db 3 EKAKFEAYKAAAAA 17
 |||:|||||
 RESULT 9
 ABP52291
 ID ABP52291 standard; peptide; 15 AA.
 XX
 AC ABP52291;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;

XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 74.4%; Score 61; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0058;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 EKAKYEAYKAAAAA 15
 |||:|||||
 Db 1 EKPKYEAYKAAAAA 15
 |||:|||||
 RESULT 10
 ABP52263
 ID ABP52263 standard; peptide; 15 AA.
 XX
 AC ABP52263;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:57.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX Example 1; Page 33; 54pp; English.
 PS
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 CC Sequence 15 AA;
 SQ
 Query Match 74.4%; Score 61; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0058;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EKAKEYAKRAAAAAA 15
 DB 1 EKAKEYAKRAAAAAA 15
 RESULT 11
 ABP52272
 ID ABP52272 standard; peptide; 15 AA.
 AC
 XX APP52272;
 DT 16-OCT-2002 (first entry)
 DE HLA-DR2 molecule binding peptide SEQ ID NO:66.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 CC Sequence 15 AA;
 SQ
 Query Match 73.2%; Score 60; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0084;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKAKEYAKRAAAAAA 15
 DB 1 EKAKEYAKRAAAAAA 15
 RESULT 12
 ABP52259
 ID ABP52259 standard; peptide; 15 AA.
 AC
 XX APP52259;
 DT 16-OCT-2002 (first entry)
 DE HLA-DR2 molecule binding peptide SEQ ID NO:53.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Example 1; Page 33; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 72.0%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
DB 1 EKAKYEAYKAAAAA 15
RESULT 13
ABP52257
ID ABP52257 standard; peptide; 15 AA.
XX
AC ABP52257;
XX
DT 16-OCT-2002 (first entry)
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200259143-A2.
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Example 1; Page 32; 54pp; English.
XX
PS The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 72.0%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.012;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
DB 1 EKAKYEAYKAAAAA 15
RESULT 14
ABP52302
ID ABP52302 standard; peptide; 17 AA.
XX
AC ABP52302;
XX
DT 16-OCT-2002 (first entry)
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; anti-inflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200259143-A2.
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
PS The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has anti-inflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 70.7%; Score 58; DB 5; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAAAA 15
DB 3 EKAKYEAYKAAAAA 17

```

RESULT 15
ABP52297 standard; peptide; 15 AA.
ID ABP52297
XX
XX ABP52297;
AC
XX 16-OCT-2002 (first entry)
DT
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:91.
DE
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX 01-AUG-2002.
PD
XX 24-JAN-2002; 2002WO-US002071.
PE
XX 24-JAN-2001; 2001US-0263569P.
PR
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 69.5%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.025;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EKAKYEAYRAAAAA 15
DB 1 EKPKFEAYRAAAAA 15

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Search completed: February 26, 2005, 23:48:23
 Job time : 87.9082 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 22.7245 Seconds
(without alignments)
55.844 Million cell updates/sec

Title: US-10-056-583A-90
Perfect score: 82
Sequence: 1 EKAKYKAYKAAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	54.9	1001	4	US-09-248-796A-18658
2	44.5	54.3	219	4	US-09-902-540-16623
3	44	53.7	405	4	US-09-328-352-4239
4	43	52.4	55	4	US-09-902-540-9849
5	43	52.4	172	4	US-09-902-540-13256
6	42	51.2	13	5	PCT-US95-04121-38
7	42	51.2	318	4	US-09-270-767-45996
8	41	50.0	102	4	US-09-101-751A-90
9	41	50.0	118	4	US-09-101-751A-46
10	41	50.0	218	4	US-09-101-751A-48
11	41	50.0	287	3	US-09-105-697-7
12	41	50.0	287	3	US-09-105-697-8
13	41	50.0	288	3	US-09-105-697-3
14	41	50.0	291	3	US-09-105-697-4
15	41	50.0	291	3	US-09-105-697-5
16	41	50.0	291	3	US-09-105-697-6
17	41	50.0	402	4	US-09-248-796A-17859
18	41	50.0	759	4	US-09-328-352-4241
19	41	50.0	830	1	US-07-977-434-6
20	41	50.0	830	1	US-08-458-819-6
21	41	50.0	830	5	PCT-US91-07035-6
22	41	50.0	831	1	US-08-073-384C-5
23	41	50.0	831	1	US-08-254-359A-5
24	41	50.0	831	1	US-08-483-043-5
25	41	50.0	831	1	US-08-483-238-5
26	41	50.0	831	2	US-08-471-066B-5
27	41	50.0	831	2	US-08-484-956-5

28	41	50.0	831	2	US-08-757-653-5	Sequence 5, Appli
29	41	50.0	831	2	US-08-599-491-5	Sequence 5, Appli
30	41	50.0	831	2	US-08-756-386-5	Sequence 5, Appli
31	41	50.0	831	2	US-08-823-516-5	Sequence 5, Appli
32	41	50.0	831	3	US-08-682-853A-5	Sequence 5, Appli
33	41	50.0	831	3	US-08-759-038-5	Sequence 5, Appli
34	41	50.0	831	3	US-08-758-114-5	Sequence 5, Appli
35	41	50.0	831	3	US-09-350-309-5	Sequence 5, Appli
36	41	50.0	831	3	US-08-520-946-5	Sequence 5, Appli
37	41	50.0	831	4	US-09-684-938-5	Sequence 5, Appli
38	41	50.0	831	4	US-09-308-825A-5	Sequence 5, Appli
39	41	50.0	831	4	US-09-758-882B-5	Sequence 5, Appli
40	41	50.0	831	4	US-09-655-378A-5	Sequence 5, Appli
41	41	50.0	831	4	US-09-940-244-5	Sequence 5, Appli
42	41	50.0	831	4	US-09-333-145-5	Sequence 5, Appli
43	41	50.0	831	4	US-09-577-304A-5	Sequence 5, Appli
44	41	50.0	832	4	US-09-758-282B-251	Sequence 251, App
45	41	50.0	832	4	US-09-758-282B-268	Sequence 268, App

ALIGNMENTS

```
RESULT 1
US-09-248-796A-18658
Sequence 18658, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248, 796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074, 725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096, 409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18658
LENGTH: 1001
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (21)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-18658
Query Match 54.9%; Score 45; DB 4; Length 1001;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 2 KAKYKAYKAAAAAPA 17
Db 818 KAKYKAYKAAAAAPA 833
RESULT 2
US-09-902-540-16623
Sequence 16623, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902, 540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217, 883
PRIOR FILING DATE: 2000-07-10
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; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16623
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16623

Query Match          54.3%; Score 44.5; DB 4; Length 219;
Best Local Similarity 70.6%; Pred. No. 8.9;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 EKAKYEVYKAAAAAPA 17
        |||:|:|:|:|:|:|
Db       191 EKAAAEET-EAAAAAPA 206

RESULT 3
US-09-328-352-4239
; Sequence 4239, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4239
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4239

Query Match          53.7%; Score 44; DB 4; Length 405;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 AKTEAYKAAAAAPA 17
        |||:|:|:|:|:|
Db       81 AQFENAGAGAAAAAPA 95

RESULT 4
US-09-902-540-9849
; Sequence 9849, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9849
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9849

Query Match          52.4%; Score 43; DB 4; Length 55;
Best Local Similarity 52.9%; Pred. No. 3.6;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 EKAKYEVYKAAAAAPA 17
        |||:|:|:|:|:|
Db       2 ETAREQAVAAASAACPA 18
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```

RESULT 5
US-09-902-540-13256
; Sequence 13256, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13256
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13256

Query Match          52.4%; Score 43; DB 4; Length 172;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 EAYKAAAAAPA 17
        |||:|:|:|:|:|
Db       160 EAQKAKKAAAAAPA 171

RESULT 6
PCT-US95-04121-38
; Sequence 38, Application PC/TUS9504121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
; NUMBER OF SEQUENCES: 62
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04121
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222,206
; FILING DATE: April 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-38

Query Match          51.2%; Score 42; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 AKTEAYKAAAAAPA 15
```

Db 1 AAYKAAKAAAAA 13

```

RESULT 7
US-09-270-767-45996
; Sequence 45996, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Hdburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45996
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45996

```

Query Match 51.2%; Score 42; DB 4; Length 318;
 Best Local Similarity 61.5%; Pred. No. 34;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 YHAYKAAAAAPA 17
 DB 34 HPAYKGAASAPA 46

```

RESULT 8
US-09-101-751A-90
; Sequence 90, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS.
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Unknown Organism
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-90

```

Query Match 50.0%; Score 41; DB 4; Length 102;
 Best Local Similarity 58.8%; Pred. No. 15;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYKAAAAAPA 17
 DB 15 EKKRAEAAAAAPA 31

RESULT 9

```

US-09-101-751A-46
; Sequence 46, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Unknown Organism
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-46

```

Query Match 50.0%; Score 41; DB 4; Length 118;
 Best Local Similarity 58.8%; Pred. No. 17;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYKAAAAAPA 17
 DB 19 EKKRAEAAAAAPA 35

```

RESULT 10
US-09-101-751A-48
; Sequence 48, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Unknown Organism
; NAME/KEY: misc feature
; LOCATION: (..)
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence

```

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      1  CITY: Branchburg
      2  STATE: New Jersey
      3  COUNTRY: United States
      4  ZIP: 08876
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      6  COMPUTER READABLE FORM:
      7  MEDIUM TYPE: Floppy disk
      8  COMPUTER: IBM PC compatible
      9  OPERATING SYSTEM: PC-DOS/MS-DOS
     10  SOFTWARE: Patent Release #1.0, Version #1.25
     11  CURRENT APPLICATION DATA:
     12  APPLICATION NUMBER: US/09/105,697
     13  FILING DATE:
     14  CLASSIFICATION:
     15  ATTORNEY/AGENT INFORMATION:
     16  NAME: Petry Ph.D., Douglas A.
     17  REGISTRATION NUMBER: 35321
     18  REFERENCE/DOCKET NUMBER: 1043
     19  TELECOMMUNICATION INFORMATION:
     20  TELEPHONE: (510) 814-2974
     21  TELEFAX: (510) 814-2974
     22  INFORMATION FOR SEQ ID NO: 8:
     23  SEQUENCE CHARACTERISTICS:
     24  LENGTH: 287 amino acids
     25  TYPE: amino acid
     26  STRANDEDNESS: single
     27  TOPOLOGY: linear
     28  MOLECULE TYPE: protein
     29  US-09-105-697-8
     30
     31  Query Match 50.0%; Score 41; DB 3; Length 287;
     32  Best Local Similarity 66.7%; Pred. No. 44;
     33  Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0
     34
     35  QY 5 YEAYKAAAP 16
     36      |||||
     37  Db 75 YEAYKAGRAP 86
     38
     39  RESULT 13
     40  US-09-105-697-3
     41  Sequence 3, Application US/09105697
     42  Patent No. 6228628
     43  GENERAL INFORMATION:
     44  APPLICANT: Gelfand Ph.D., David H.
     45  APPLICANT: Reichert, Fred L.
     46  TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
     47  NUMBER OF SEQUENCES: 11
     48  CORRESPONDENCE ADDRESS:
     49  ADDRESSEE: Roche Molecular Systems
     50  STREET: 1080 U.S. Highway 202
     51  CITY: Branchburg
     52  STATE: New Jersey
     53  COUNTRY: United States
     54  ZIP: 08876
     55  COMPUTER READABLE FORM:
     56  MEDIUM TYPE: Floppy disk
     57  COMPUTER: IBM PC compatible
     58  OPERATING SYSTEM: PC-DOS/MS-DOS
     59  SOFTWARE: Patent Release #1.0, Version #1.25
     60  CURRENT APPLICATION DATA:
     61  APPLICATION NUMBER: US/09/105,697
     62  FILING DATE:
     63  CLASSIFICATION:
     64  ATTORNEY/AGENT INFORMATION:
     65  NAME: Petry Ph.D., Douglas A.
     66  REGISTRATION NUMBER: 35321
     67  REFERENCE/DOCKET NUMBER: 1043
     68  TELECOMMUNICATION INFORMATION:
     69  TELEPHONE: (510) 814-2974
     70  TELEFAX: (510) 814-2974
     71  INFORMATION FOR SEQ ID NO: 3:
     72  SEQUENCE CHARACTERISTICS:
     73  LENGTH: 288 amino acids

```


TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-3

Query Match 50.0%; Score 41; DB 3; Length 288;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAP 16
| | | | | | | |
Db 79 YEAYKAGRAP 88

RESULT 14

US-09-105-697-4
Sequence 4, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-4

Query Match 50.0%; Score 41; DB 3; Length 291;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAP 16
| | | | | | | |
Db 79 YEAYKAGRAP 90

RESULT 15

US-09-105-697-5
Sequence 5, Application US/09105697
Patent No. 6228628
GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-697-5

Query Match 50.0%; Score 41; DB 3; Length 291;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAP 16
| | | | | | | |
Db 79 YEAYKAGRAP 90

Search completed: February 26, 2005, 23:59:29
Job time : 22.7245 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 60.7143 Seconds
(without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583A-90

Perfect score: 82

Sequence: 1 EKAKYEAYKAAAAAPA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

1385339

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubppa/PCr_NEW_PUB.pep:*

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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	82	100.0	17	US-10-056-583-90
2	82	100.0	19	US-10-056-583-89
3	82	100.0	15	US-10-056-583-88
4	82	100.0	15	US-10-056-583-87
5	82	100.0	15	US-10-056-583-86
6	82	100.0	15	US-10-056-583-85
7	82	100.0	15	US-10-056-583-84
8	82	100.0	15	US-10-056-583-83
9	82	100.0	15	US-10-056-583-82
10	82	100.0	15	US-10-056-583-81
11	82	100.0	15	US-10-056-583-80
12	82	100.0	15	US-10-056-583-79
13	82	100.0	15	US-10-056-583-78

14	58	70.7	17	US-10-056-583-96	Sequence 96, Appl
15	57	69.5	15	US-10-056-583-91	Sequence 91, Appl
16	56	68.3	15	US-10-056-583-33	Sequence 33, Appl
17	56	68.3	15	US-10-056-583-43	Sequence 43, Appl
18	56	68.3	15	US-10-056-583-47	Sequence 47, Appl
19	55	67.1	15	US-10-056-583-38	Sequence 38, Appl
20	55	67.1	15	US-10-056-583-55	Sequence 55, Appl
21	55	67.1	15	US-10-056-583-56	Sequence 56, Appl
22	55	67.1	15	US-10-056-583-63	Sequence 63, Appl
23	55	67.1	15	US-10-056-583-83	Sequence 83, Appl
24	55	67.1	15	US-10-056-583-86	Sequence 86, Appl
25	54	65.9	15	US-10-056-583-30	Sequence 30, Appl
26	54	65.9	15	US-10-056-583-38	Sequence 38, Appl
27	54	65.9	15	US-10-056-583-58	Sequence 58, Appl
28	53	64.6	15	US-10-056-583-61	Sequence 61, Appl
29	52	63.4	15	US-10-056-583-93	Sequence 93, Appl
30	51	62.2	15	US-10-056-583-59	Sequence 59, Appl
31	51	62.2	15	US-10-056-583-34	Sequence 34, Appl
32	51	62.2	15	US-10-056-583-35	Sequence 35, Appl
33	51	62.2	15	US-10-056-583-42	Sequence 42, Appl
34	51	62.2	15	US-10-056-583-43	Sequence 43, Appl
35	51	62.2	15	US-10-056-583-48	Sequence 48, Appl
36	51	62.2	15	US-10-056-583-49	Sequence 49, Appl
37	50	61.0	15	US-10-056-583-98	Sequence 98, Appl
38	50	61.0	15	US-10-056-583-25	Sequence 25, Appl
39	50	61.0	15	US-10-056-583-26	Sequence 26, Appl
40	49	59.8	15	US-10-056-583-62	Sequence 62, Appl
41	49	59.8	15	US-10-056-583-29	Sequence 29, Appl
42	48	58.5	15	US-10-056-583-44	Sequence 44, Appl
43	48	58.5	15	US-09-765-301-19	Sequence 19, Appl
44	48	58.5	15	US-09-765-644A-19	Sequence 19, Appl
45	48	58.5	15	US-10-056-583-32	Sequence 32, Appl
			15	US-10-056-583-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-10-056-583-90

Sequence 90, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Fiddis-Harell, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DENEUTELINATING

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 90

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-90

Query Match 100.0%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAAPA 17
DB 1 EKAKYEAYKAAAAAPA 17

RESULT 2

US-10-056-583-89

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/ Sequence 89, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 89
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

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Query Match      100.0%; Score 82; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKRAAAAAA 17
         |||||
Db       3 EKAKEYAYKRAAAAAA 19
```

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RESULT 3
US-10-056-583-65:
/ Sequence 65, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 65
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

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Query Match      86.6%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKRAAAAAA 15
         |||||
Db       1 EKAKEYAYKRAAAAAA 15
```

```
RESULT 4
US-10-056-583-88
/ Sequence 88, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
```

```
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 88
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match      86.6%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYAYKRAAAAAA 15
         |||||
Db       3 EKAKEYAYKRAAAAAA 17
```

```
RESULT 5
US-10-056-583-64
/ Sequence 64, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 60/263,569
/ PRIOR FILING DATE: 2001-01-24
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
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Query Match      79.3%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 EKAKEYAYKRAAAAAA 15
         |||||
Db       1 EKAKEYAYKRAAAAAA 15
```

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RESULT 6
US-10-056-583-95
/ Sequence 95, Application US/10056583
/ Publication No. US20030064915A1
/ GENERAL INFORMATION:
/ APPLICANT: Presidents and Fellows of Harvard College
/ APPLICANT: Strominger, Jack L.
/ APPLICANT: Fridkis-Hareli, Masha
/ TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
/ FILE REFERENCE: 24655-017
/ CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match          76.8%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EKATYEAAYKAAAAA 15
Db      1 EKAKFEAFKAAAAA 15

RESULT 7
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match          75.6%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0036;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKATYEAAYKAAAAA 15
Db      1 EKAKFEAYKAAAAA 15

RESULT 8
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match          75.6%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0041;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKATYEAAYKAAAAA 15
Db      3 EKAKFEAYKAAAAA 17

RESULT 9
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match          74.4%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0051;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKATYEAAYKAAAAA 15
Db      1 EKAKYAAAYKAAAAA 15

RESULT 10
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match 74.4%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0051;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 1 EKPKYEAYKAAAAA 15

RESULT 11
US-10-056-583-66

; Sequence 66; Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 73.2%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0074;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 1 EAKKYEAYKAAAAA 15

RESULT 12
US-10-056-583-51;
; Sequence 51; Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 1 EAKKYEAYKAAAAA 15

RESULT 13
US-10-056-583-96

; Sequence 96; Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53

Query Match 72.0%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 1 EKAAYAYKAAAAA 15

RESULT 14
US-10-056-583-96
; Sequence 96; Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match 70.7%; Score 58; DB 14; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 3 EKAKEFAKAAAAA 17

Query Match 72.0%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.011;

RESULT 15

US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match 69.5%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
Db 1 EKPKFEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:23
Job time : 60.7143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 15.0918 seconds
(without alignments)
108.382 Million cell updates/sec

Title: US-10-056-583a-90

Perfect score: 82
Sequence: 1 EKAKYKAYKAAAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	57.3	108	2 F97521	VCO33 protein homo
2	47	57.3	108	2 AH2740	conserved hypochet
3	46	56.1	339	2 S39979	chitinase (EC 3.2.
4	46	56.1	340	2 S40414	chitinase (EC 3.2.
5	45	54.9	188	2 T50145	homeotic protein H
6	45	54.9	289	2 A43562	homeotic protein H
7	44	53.7	270	2 T31225	trif protein homol
8	44	53.7	282	2 T51013	related to calmodu
9	44	53.7	398	2 T21061	hypothetical prote
10	44	53.7	503	1 VKUT1B	variant surface gl
11	43	52.4	49	2 PX0029	protein C inhibito
12	43	52.4	176	2 G87606	transcription regu
13	43	52.4	179	2 F97683	50S ribosomal prot
14	43	52.4	179	2 AF2908	50S ribosomal prot
15	43	52.4	185	2 S36290	T-cell receptor ga
16	43	52.4	379	2 T08277	carotenoid biosynt
17	43	52.4	441	2 A43555	GAP-43-related pro
18	43	52.4	736	2 D96830	probable heat-shoc
19	42	51.2	200	2 T48130	hypothetical prote
20	42	51.2	318	2 B48487	MOCB (Tn4399) - Ba
21	42	51.2	698	2 T32594	hypothetical prote
22	42	51.2	748	2 S61247	DNA helicase/prima
23	42	51.2	2957	2 T33152	hypothetical prote
24	41.5	50.6	189	2 S77930	exoskeletal protei
25	41.5	50.6	189	2 S77935	exoskeletal protei
26	41	50.0	113	2 T30041	trans-activating t
27	41	50.0	129	2 TNLJG3	ribosomal protein
28	41	50.0	165	2 B87702	hypothetical prote
29	41	50.0	166	2 T34804	hypothetical prote

30	41	50.0	177	2 AD1307	peptidyl methionin
31	41	50.0	177	2 AD1679	peptidyl methionin
32	41	50.0	192	1 MOCHIA	myosin alkali ligh
33	41	50.0	254	2 H86355	probable 14-3-3 pr
34	41	50.0	421	2 JV0057	to1a protein - Bsc
35	41	50.0	470	2 AF2828	FAD dependent oxid
36	41	50.0	477	2 D97606	glycolate oxidase
37	41	50.0	521	2 T49355	related to protein
38	41	50.0	571	2 XZAD32	penton protein (II
39	41	50.0	571	1 XZADH5	penton protein (II
40	41	50.0	641	2 PH1919	FL-160-4 protein -
41	41	50.0	831	2 S26675	DNA-directed DNA p
42	41	50.0	1885	1 JC4086	fatty-acid synthas
43	41	50.0	2129	2 T27431	hypothetical prote
44	40.5	49.4	151	2 D87276	hypothetical prote
45	40.5	49.4	1655	2 T32633	hypothetical prote

ALIGNMENTS

RESULT 1
F97521
VCO33 protein homolog (AF179595) [imported] - Agrobacterium tumefaciens (strain C58, Ce
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97521
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F97521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8UFR1; GB:AE007869; PIDD:AK87127.1; PIDD:G15156391; GSPDB:
C:Genetics:
A:Gene: AGR_C_2462
A:Map position: circular chromosome

Query Match 57.3% Score 47; DB 2; Length 108;
Best local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKYKAYKAAAAAPA 17
DB 60 AAYEAYKARLAADPA 74

RESULT 2
AH2740
conserved hypothetical protein Atul136 [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AH2740
R:Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McEl
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8UFR1; GB:AE008688; PIDD:AL42342.1; PIDD:G17739747; GSPDB:
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atul136
A:Map position: circular chromosome

Query Match 57.3%; Score 47; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 2.6;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKYAYKAAKAAAPA 17
 |||||:|||||
 Db 60 AYAYTRARLAAAPA 74

RESULT 3

chitinase (EC 3.2.1.14) - rice
 S39979
 C/Species: Oryza sativa (rice)
 C/Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S39979
 R/Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibl, T.
 Mol. Gen. Genet. 241, 1-10, 1993
 A/Title: Sequence variation, differential expression and chromosomal location of rice chitinase
 A/Reference number: S39979; MUID:94049667; PMID:7901749
 A/Accession: S39979
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-339 <NIS>
 A/Cross-references: UNIPROT:Q43294; EMBL:X56787
 C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 F/33-74/Domain: hevein chitin-binding domain homology <HCB>
 F/91-329/Domain: plant chitinase homology <PCH>

Query Match 56.1%; Score 46; DB 2; Length 339;
 Best Local Similarity 76.9%; Pred. No. 11;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAKAAAPA 17
 |||||:|||||
 Db 117 YEAFIAAAAPPA 129

RESULT 4

chitinase (EC 3.2.1.14) - rice
 S40414
 C/Species: Oryza sativa (rice)
 C/Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S40414
 R/Nishizawa, Y.
 Submitted to the EMBL Data Library, November 1990
 A/Reference number: S40414
 A/Accession: S40414
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-340 <NIS>
 A/Cross-references: UNIPROT:Q43294; EMBL:X56787; NID:9407471; PIDN:CAA0107.1; PID:94074
 C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation
 F/33-74/Domain: hevein chitin-binding domain homology <HCB>
 F/92-330/Domain: plant chitinase homology <PCH>

Query Match 56.1%; Score 46; DB 2; Length 340;
 Best Local Similarity 76.9%; Pred. No. 11;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAKAAAPA 17
 |||||:|||||
 Db 118 YEAFIAAAAPPA 130

RESULT 5

homeotic protein Hox M - chicken
 IS0145
 N/Alternate names: CHOX M
 C/Species: Gallus gallus (chicken)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

C/Accession: IS0145; S14512
 R/Crompton, M.R.; Macgregor, A.D.; Goodwin, G.H.
 Leukemia 5, 357-360, 1991

A/Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vira
 A/Reference number: IS0145; MUID:91238215; PMID:1674560
 A/Accession: IS0145
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-188 <CRO>
 A/Cross-references: UNIPROT:P23459; EMBL:X57158; NID:962700; PIDN:CAA040445.1; PID:962701
 C/Genetics:
 A/Gene: CHOX M
 C/Superfamily: homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/96-152/Domain: homeobox homology <HOB>

Query Match 54.9%; Score 45; DB 2; Length 188;
 Best Local Similarity 76.9%; Pred. No. 8;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YEAYKAAKAAAPA 17
 |||||:|||||
 Db 10 YSKYKAAKAAAPPA 22

RESULT 6

homeotic protein Hox DB - mouse
 A43562
 N/Alternate names: homeotic protein Hox 4.3
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
 C/Accession: A43562
 R/Zipf, A.; Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubot
 Development 110, 733-745, 1990
 A/Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc
 A/Reference number: A43562; MUID:91209232; PMID:1982431
 A/Accession: A43562
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-289 <IZP>
 A/Cross-references: UNIPROT:P23463
 C/Superfamily: homeotic protein Hox A7; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/196-252/Domain: homeobox homology <HOB>

Query Match 54.9%; Score 45; DB 2; Length 289;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YEAYKAAKAAAPA 17
 |||||:|||||
 Db 10 YSKYKAAKAAAPPA 22

RESULT 7

traf protein homolog - Sphingomonas aromaticivorans plasmid pNLI
 T31225
 C/Species: Sphingomonas aromaticivorans
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T31225
 R/Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sengen, C.W.; C
 Submitted to the EMBL Data Library, July 1998
 A/Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
 A/Reference number: Z20992
 A/Accession: T31225
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-270 <ROM>
 A/Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:93378261; PID:93378366; PIDN:AAD
 C/Genetics:
 A/Genome: plasmid pNLI
 A/Note: traf

```

Query Match 53.7% Score 44; DB 2; Length 270;
Best Local Similarity 64.7% Pred. No. 18;
Matches 11; Conservative 0; Mismatches 6; Indels 0;

QY 1 EKAKYEAYKAAAAAPA 17
DB 54 EKPKKEPRKAAAAQPPA 70

RESULT 8
T51013
related to calmodulin-binding protein [imported] - Neurospora crassa
N.Alternate names: protein B7J19.120
C.Species: Neurospora crassa
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C.Accession: T51013
R.Schultze, U.; Aigai, V.; Hohsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A.Reference number: Z25286
A.Accession: T51013
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-282 <SCH>
A.Cross-references: EMBL:AL389899; GSPDB:GN00116; NCSP:B7J19.120
A.Experimental source: BAC clone B7J19; strain OR74A
C.Genetics:
A.Gene: NCSP:B7J19.120
A.Map position: 6

Query Match 53.7% Score 44; DB 2; Length 282;
Best Local Similarity 73.3% Pred. No. 18;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAAPA 17
DB 197 AKQKALAAAAAPA 211

RESULT 9
T21061
hypothetical protein F17C11.9 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T21061
R.McMurray, A.
submitted to the EMBL Data Library, May 1996
A.Reference number: Z19366
A.Accession: T21061
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-398 <WII>
A.Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDD:CAA96631.1; GSPDB:GN00023; CESP:F
A.Experimental source: clone F17C11
C.Genetics:
A.Gene: CESP:F17C11.9
A.Map position: 5
A.Introns: 3/3; 44/3; 151/3; 196/1; 354/3
C.Superfamily: translation elongation factor eEF-1 gamma chain

Query Match 53.7% Score 44; DB 2; Length 398;
Best Local Similarity 68.8% Pred. No. 25;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAAP 16
DB 214 EKPKKEAPKAAAAAP 229

RESULT 10
VMUT1B
variant surface glycoprotein Antra 1.1 precursor - Trypanosoma brucei brucei
C.Species: Trypanosoma brucei brucei
C.Date: 31-Mar-1999 #sequence_revision 31-Mar-1999 #text_change 09-Jul-2004

```

```

C:Accession: S07174; S18522; S09253; S10844
R:Michiels, F.; Matthyssens, G.; Kronenberger, P.; Pays, E.; Dero, B.; van Assel, S.; D
EMBO J. 2, 1185-1192, 1983
A:Title: Gene activation and re-expression of a Trypanosoma brucei variant glyco
A:Reference number: S07174; MUID:64028590; PMID:6313354
A:Accession: S07174
A:Molecule type: DNA
A:Residues: 1-503 <MTC>
A:Cross-references: UNIPROT:P06015, EMBL:X01843, NID:G10429, PIDN:CAA25971.1, PID:G1043
A:Accession: S18522
A:Molecule type: mRNA
A:Residues: 1-503 <MTC>
A:Cross-references: GB:X01843, NID:G10429, PIDN:CAA25971.1, PID:G10430
A:Note: part of this sequence, including the amino end of the mature protein, was confi
R:van der Werf, A.; van Assel, S.; Aerts, D.; Steinert, M.; Pays, E.
EMBO J. 9, 1035-1040, 1990
A:Title: Telomere interactions may condition the programming of antigen expression in T
A:Reference number: S09252; MUID:90214610; PMID:2323332
A:Accession: S09253
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-333, 'P', 335-345, 'V', 347-416 <VAN>
A:Cross-references: EMBL:X15817, NID:G10381, PIDN:CAA33809.1, PID:G10382
R:Matthyssens, G.; Michiels, F.; Hamers, R.; Pays, E.; Steinert, M.
Nature 293, 230-233, 1981
A:Title: Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-ter
A:Reference number: A17609; MUID:82013622; PMID:7278981
A:Accession: S10844
A:Molecule type: mRNA
A:Residues: 351-418, 'K', 420-503 <MATH>
A:Cross-references: EMBL:J01213, NID:G162361, PIDN:AAA30280.1, PID:G162362
A:Note: the authors translated the codon AAG for residue 419 as Asn and TTC for residue
C:Superfamily: variant surface glycoprotein
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat
F:1-30/Domains: signal sequence #status predicted <SIG>
F:331-480/Product: variant surface glycoprotein Antat 1.1 #status experimental <MAT>
F:113, 419, 432/Binding site: carboxyl-terminal propenptide #status predicted <CTP>
F:1480/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)
Query Match 53.7%; Score 44; DB 1; Length 503;
Best Local Similarity 56.2%; Pred. No. 31;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKATKAYKAAAAAP 16
Db 427 KKCKTNATKASADAP 442

RESULT 11
PK0029
protein C inhibitor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PK0029
R:Suzuki, K.; Kusumoto, H.; Nishioaka, J.; Komiyama, Y.
J. Biochem. 107, 381-388, 1990
A:Title: Bovine plasma protein C inhibitor with structural and functional homologous pr
A:Reference number: PK0029; MUID:90256711; PMID:2160449
A:Accession: PK0029
A:Molecule type: protein
A:Residues: 1-49 <SUZ>
A:Cross-references: UNIPROT:Q9N212
A:Experimental source: plasma
A:Superfamily: Serpin

Query Match 52.4%; Score 43; DB 2; Length 49;
Best Local Similarity 61.5%; Pred. No. 5.2;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEATKAAAAAAP 17
Db 27 FDLTRALAAAAAP 39

```

RESULT 12

G87606

transcription regulator, Aenc family [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C/Accession: G87606

R/Nerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of *Caulobacter crescentus*.

A/Reference number: A87249; MUID:21173698; PMID:11259647

A/Accession: G87606

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-176 <STO>

A/Cross-references: UNIPROT:Q9A4E7; GB:AE005673; NID:g13424505; PIDN:AAK24851.1; GSPDB:C

A/Genetic:

A/Gene: CC2887

C/Superfamily: regulatory protein asnc

Query Match 52.4%; Score 43; DB 2; Length 176;

Best Local Similarity 52.9%; Pred. No. 17;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAAPAA 17

Db 99 EFARYEAFEAVALRHAPA 115

RESULT 13

F97683

50S ribosomal protein L19 [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)
C/Species: *Agrobacterium tumefaciens*

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C/Accession: F97683

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: F97683

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-179 <KUR>

A/Cross-references: UNIPROT:Q8UBZ5; GB:AB007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:C

C/Genetics:

A/Gene: AGR_C_4900

A/Map position: circular chromosome

C/Superfamily: Escherichia coli ribosomal protein L19

Query Match 52.4%; Score 43; DB 2; Length 179;

Best Local Similarity 64.7%; Pred. No. 17;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAAPAA 17

Db 137 EKARLEAEKVAQAALAA 153

RESULT 14

AF2908

50S ribosomal protein L19 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C/Species: *Agrobacterium tumefaciens*

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AF2908

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moe, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCell

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AF2908

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-179 <KUR>

A/Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAK43684.1; PID:g17741210; GSPDB:C

A/Experimental source: strain C58 (Dupont)

A/Genetics:

A/Gene: rplS

A/Map position: circular chromosome

C/Superfamily: Escherichia coli ribosomal protein L19

Query Match 52.4%; Score 43; DB 2; Length 179;

Best Local Similarity 64.7%; Pred. No. 17;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAAPAA 17

Db 137 EKARLEAEKVAQAALAA 153

RESULT 15

S36290

T-cell receptor gamma chain precursor - sheep (fragment)

C/Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C/Accession: S36290; S23041

R/Hein, W.R.; Dudley, L.

EMBO J. 12, 715-724, 1993

A/Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta

A/Reference number: S36287; MUID:93178447; PMID:8440261

A/Accession: S36290

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-185 <HEI>

A/Cross-references: EMBL:Z12998; NID:g2260; PIDN:CAA78342.1; PID:g2261

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 52.4%; Score 43; DB 2; Length 185;

Best Local Similarity 66.7%; Pred. No. 18;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAAYKAAA 12

Db 81 DKAKYSVYKGA 92

Search completed: February 26, 2005, 23:57:16
Job time : 16.0918 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 73.898 Seconds

(without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583A-90

Perfect score: 82

Sequence: 1 EKAKYEAAYKAAAAAPA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	58.5	300	2	09VFL4
2	48	58.5	463	2	09VFL4
3	47	57.3	108	2	08UFR1
4	47	57.3	110	2	098DQ0
5	46	56.1	340	2	043294
6	46	56.1	340	2	07DNA1
7	45.5	55.5	457	2	094DE6
8	45	54.9	151	2	063KJ9
9	45	54.9	188	1	HXD8_CHICK
10	45	54.9	289	1	HXD8_MOUSE
11	45	54.9	289	2	081XZ1
12	45	54.9	290	1	HXD8_HUMAN
13	45	54.9	707	2	064CB3
14	45	54.9	949	2	082K16
15	44	53.7	71	2	09M3P6
16	44	53.7	158	2	09M3Q7
17	44	53.7	232	2	084YW5
18	44	53.7	270	2	0942W3
19	44	53.7	270	2	0859J3
20	44	53.7	274	2	0874I3
21	44	53.7	274	2	09VFL3
22	44	53.7	282	2	07SCA9
23	44	53.7	299	2	06YSU4
24	44	53.7	356	2	06ZAU1
25	44	53.7	373	2	081AK9
26	44	53.7	398	1	FRIG_CAEEL
27	44	53.7	403	1	QZNZ81
28	44	53.7	677	2	VSAL_TRYBB
29	44	53.7	71	2	064NFB
30	43	52.4	71	2	09M3Q4
31	43	52.4	71	2	09M3Q6

32	43	52.4	176	2	09A4E7	Q9A4E7 caulobacter
33	43	52.4	177	1	RL19_RHME	Q92139 rhizobium m
34	43	52.4	179	1	RL19_AGR75	Q92139 agrobacteri
35	43	52.4	181	1	RL19_RH10	P58166 rhizobium i
36	43	52.4	220	2	070M24	Q70M24 halotribum
37	43	52.4	223	2	070M29	Q70M29 halobacteri
38	43	52.4	225	2	070M27	Q70M27 halobacteri
39	43	52.4	227	2	067M05	Q67M05 symbiobacte
40	43	52.4	232	2	09ZTR8	Q9ZTR8 hordeum vul
41	43	52.4	241	2	091ZP6	Q91ZP6 m nedda4 ww
42	43	52.4	241	2	08BVCS	Q8BVCS mus musculi
43	43	52.4	241	2	061R02	Q61R02 mus musculi
44	43	52.4	299	1	RL22_DROME	P50887 drosophila
45	43	52.4	312	2	Q9UAN1	Q9UAN1 drosophila

ALIGNMENTS

RESULT 1	ID	Q9VFL4	PRELIMINARY;	PRT;	300 AA.
AC	Q9VFL4				
DT	01-MAY-2000	(TREMBlrel. 13, Created)			
DT	01-MAY-2000	(TREMBlrel. 13, Last sequence update)			
DT	25-OCT-2004	(TREMBlrel. 28, Last annotation update)			
DE	CG14840-PA	(AT18408P).			
GN	ORFNames=CG14840;				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OK	NCBI_taxid=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.H., Blazek R.G., Champ M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,				
RA	Abell J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,				
RA	Botkova D., Botchan M.R., Bouck J., Breckstein P., Brothier P.,				
RA	Burtis K.C., Bussam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,				
RA	Jatani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkllov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,				
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,				
RA	Snie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,				
RA	Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,				
RA	Syrakasas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,				
RA	Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,				
RA	Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,				
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				
RA	Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,				
RT	"The genome sequence of Drosophila melanogaster."				

RL Science 287.2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminher J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminher J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu J., Berman B.P.,
 RA Battecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY003704; AAF55038.1; -;
 DR EMBL; AY089356; AAL90094.1; -;
 DR Inctac; Q9VF4; -;
 DR FlyBase; FBGN0038217; CG14840.
 DR InterPro; IPR007999; DUF745.
 DR Pfam; PF05355; DUF745; 1.
 SQ SEQUENCE 300 AA; 31262 MW; 67D1586B3044A8FC CRC64;
 Query Match 58.5%; Score 48; DB 2; Length 300;
 Best Local Similarity 64.7%; Pred. No. 28;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE CG6301-Pa.
 GN ORFNames=CG6301;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.H., Blazek R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benoe P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Dou P.L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Fosler A., Gong F., Gorrie J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287.2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminher J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2426069; PubMed=12531752;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smuth C.D., Tupy J.L., Whitfield B.J., Bayraktiroglu U., Berman B.P.,
 RA Batecourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003805; AAF57947.2; -.
 DR InFACt; Q9V7U6; -.
 DR FlyBase; FBgn0034161; CG6301.
 DR InterPro; IPR007999; DUF745.
 DR Pfam; PF05335; DUF745; 1.
 SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEFBEBC9 CRC64;

Query Match 58.5%; Score 48; DB 2; Length 463;
 Best Local Similarity 64.7%; Pred. No. 42;
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AKYEAYKAAAPAA 17
 Db 275 EKTQAAAYKAAAPAA 291

RESULT 3

OBUPRI PRELIMINARY; PRT; 108 AA.

AC Q8UFR1; Q7CZH4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein Atu1336 (AGR_C2462p).
 GN OrderedLocustNames=AGR_C2462, Atu1336; / ATCC 33970).
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;
 RA MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitejima J.P.,
 RA Okura V.R., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
 RA Chapman P., Clendinning J., Decherage G., Gillet W., Grant C.,
 RA Kutyavin T., Levy R., Li M.-U., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krepan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chunley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.,
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cereoni;
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gactung S., Miller N., Blanchard M.,
 RA Ouroulo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
 RA Hounmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,
 RA Pianegan C., Crowell C., Guron J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58."
 RL Science 294:2323-2328(2001).
 DR EMBL; AB009095; AAL42342.1; -.
 DR EMBL; AB008059; AAK87127.1; -.
 DR PIR; AH2740; AH2740.
 DR PIR; F97521; F97521.
 DR InterPro; IPR011008; Dimer A_B_barrel.
 DR InterPro; IPR009478; DUF1099.
 DR Pfam; PF06499; DUF1099; 1.
 KM Hypothetical protein: Complete proteome.
 SQ SEQUENCE 108 AA; 12371 MW; A48C7CB4BC2BD3A CRC64;

Query Match 57.3%; Score 47; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 4

Q98D00 PRELIMINARY; PRT; 110 AA.

AC Q98D00;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE M114604 protein.
 GN OrderedLocustNames=m114604;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
 RA Wochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT *Mesorhizobium loti*."
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003004; BAB51220.1; -.
 DR InterPro; IPR009478; DUF1099.
 DR Pfam; PF06499; DUF1099; 1.
 KM Complete proteome.
 SQ SEQUENCE 110 AA; 12441 MW; F41FP0DEB3CA8885 CRC64;

Query Match 57.3%; Score 47; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AKYEAYKAAAPAA 17
 Db 61 AA YEAYKAAAPAA 75

RESULT 5

Q43294 PRELIMINARY; PRT; 340 AA.

AC Q43294;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Chitinase precursor (BC 3.2.1.14).

```

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthroideae; Oryzeae; Oryza.
OC NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japonica;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes.";
RL Møl. Gen. Genet. 241:1-10(1993).
DR EMBL; X56787; CAA40107.1; -.
DR PIR; S39979; S39979.
DR PIR; S40414; S40414.
DR HSSP; P23951; ICNS.
DR Gramene; Q43294; -.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001002; Chitin_binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR PRODOM; PD000609; Chitin_binding_1; 1.
DR PRODOM; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChEBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
DR Chitin-binding; Glycosidase; Hydrolyase; Signal.
FT SIGNAL 1 340
FT CHAIN 33 340
FT CHAIN 33 340
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 56.1%; Score 46; DB 2; Length 340;
Best Local Similarity 76.9%; Pred. No. 65;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 5 YEAYKAAAAAPPA 17
DB 118 YEAFLLAAAAAPPA 130

RESULT 6
ID Q7DNA1 PRELIMINARY; PRT; 340 AA.
AC Q7DNA1;
DT 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Endochitinase precursor (EC:3.2.1.14).
GN Name=Chit-2;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthroideae; Oryzeae; Oryza.
OC NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes.";
RL Møl. Gen. Genet. 241:1-10(1993).
DR EMBL; D16222; BAA03750.1; -.

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DR HSSP; P10699; 1KTV.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0006032; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001002; Chitin_binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR PRODOM; PD000609; Chitin_binding_1; 1.
DR PRODOM; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChEBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
DR Chitin-binding; Glycosidase; Hydrolyase; Signal.
FT SIGNAL 1 340
FT CHAIN 33 340
FT CHAIN 33 340
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 56.1%; Score 46; DB 2; Length 340;
Best Local Similarity 76.9%; Pred. No. 65;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 5 YEAYKAAAAAPPA 17
DB 118 YEAFLLAAAAAPPA 130

RESULT 7
ID Q94DE6 PRELIMINARY; PRT; 457 AA.
AC Q94DE6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative 3-deoxy-d-manno-octulosonic-acid transferase (KDO
transferase).
GN Name=P0683P02.6; Synonyms=OJ1402_H07.14;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthroideae; Oryzeae; Oryza.
OC NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA W. J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Noki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Idojima A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaoka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yanane H., Yoshiki S., Yoshitane R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003289; BAB63703.1; -.
DR EMBL; AP003415; BAC03325.1; -.
DR Gramene; Q94DE6; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

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DR InterPro; IPR007507; Glycos_transf_N.
DR Pfam; PF04413; Glycos_transf_N; 1.
KM Transferrase.
SQ SEQUENCE 457 AA; 50371 MW; B8B6C658CB86A4D1 CRC64;

Query Match
Best Local Similarity 55.5%; Score 45.5; DB 2; Length 457;
Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 KAKTEAYKAA-AAAA 17
DB 15 RALVELYRAASRAAPA 31

RESULT 8
063KJ9 PRELIMINARY; PRT; 151 AA.
AC 063KJ9;
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Putative exported protein.
GN ORFNames=BBS1363;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bertley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Chervach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Fellwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songsvilait S., Stevens K., Tmupa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
SQ SEQUENCE 151 AA; 14873 MW; 532610BF64B35F17 CRC64;

Query Match
Best Local Similarity 54.9%; Score 45; DB 2; Length 151;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 KAKTEAYKAA-AAAA 17
DB 60 KTWYGASKAAATAP 75

RESULT 9
HXD8 CHICK STANDARD; PRT; 188 AA.
AC P23459;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Chox-M).
GN Name=HoxD8; Synonyms=CHOX-M;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=91238215; PubMed=1674560;

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RA Crompton M.R., McGregor A.D., Goodwin G.H.;
RT "cDNA cloning of a homeobox-containing gene expressed in avian
RT myeloblastic virus-transformed chicken monoblastic leukemia cells.";
RL Leukemia 5:357-360(1991).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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DR EMBL; X57158; CAA40445.1; -.
DR PIR; I50145; I50145.
DR HSBP; P02833; 9ANT.
DR TRANSFAC; T01754; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR000047; HTH_1andrepreser.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEOBOX; 1.
DR PROSITE; PS50071; HOMEOBOX 2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 25 Poly-Ala.
FT SITE 83 88 Antp-type hexapeptide.
FT DNA_BIND 95 154 Homeobox.
SQ SEQUENCE 188 AA; 21729 MW; D4560E8807FE29FE CRC64;

Query Match
Best Local Similarity 54.9%; Score 45; DB 1; Length 188;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YEAYKAA-AAAA 17
DB 10 YSKYKAA-AAAA 22

RESULT 10
HXD8 MOUSE STANDARD; PRT; 289 AA.
AC P23453;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-JUL-1993 (Rel. 46, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).
GN Name=HoxD8; Synonyms=Hox-4.3; Hoxd-8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=91209232; PubMed=1982431;
RA Teplov-Belmonte J.-C., Dollé P., Renucci A., Zappavigna V.,
RA Falkenstein H., Duboule D.;
RT "Primary structure and embryonic expression pattern of the mouse Hox-
RT 4.3 homeobox gene.";
RL Development 110:733-745(1990).

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RN [2]
 RP SEQUENCE OF 191-269 FROM N.A.
 RX MEDLINE=91274361; PubMed=16755873; DOI=10.1016/0167-4781(91)90020-M;
 RA Sadoul R., Featherstone M.;
 RT "Sequence analysis of the homeobox-containing exon of the murine Hox-
 4.3 homeogene.";
 RL Biochim. Biophys. Acta 1089:259-261 (1991).
 RN [3]
 RP SEQUENCE OF 195-254 FROM N.A.
 RX MEDLINE=92073356; PubMed=1683707;
 RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
 RT "Identification of 10 murine homeobox genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
 RN [4]
 RP SEQUENCE OF 192-260 FROM N.A.
 RX MEDLINE=92212934; PubMed=1348361;
 RA Nazareli A., Kim Y., Nirenberg M.;
 RT "Hox-1.11 and Hox-4.9 homeobox genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).
 CC -1- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the Antp homeobox family.
 CC -1- SIMILARITY: Contains 1 homeobox domain.
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 DR EMBL; X56561; CAA39911.1; -;
 DR EMBL; M87803; AA37852.1; -;
 DR PIR; A43562; A43562.
 DR PIR; S16177; A41605.
 DR HSSP; P02833; 9ANT.
 DR TRANSFAC; T01426; -;
 DR MGP; MGI:96209; Hoxd8.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeobox_in_like.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR Developmental protein; DNA-binding; Homeobox; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 15 28 Poly-Ala.
 FT DOMAIN 62 89 Gly/Pro-rich.
 FT SITE 108 117 Antp-type hexapeptide.
 FT SITE 183 188 Antp-type hexapeptide.
 FT DNA_BIND 195 254 Homeobox.
 FT CONFLICT 207 208 TL -> RV (in Ref. 1).
 FT CONFLICT 231 231 T -> S (in Ref. 1).
 FT CONFLICT 255 256 EA -> DG (in Ref. 1).
 FT CONFLICT 275 275 A -> V (in Ref. 2).
 SQ SEQUENCE 289 AA; 31410 MW; 5783099FB9B2BDFE CRC64;
 Query Match 54.9%; Score 45; DB 1; Length 289;
 Best Local Similarity 76.9%; Pred. No. 80;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
 ID 081X21 PRELIMINARY; PRT; 289 AA.
 AC 081X21.
 DT 01-MAR-2003 (TRENDEL 23, Created)
 DT 01-MAR-2003 (TRENDEL 23, Last sequence update)
 DT 01-MAR-2004 (TRENDEL 26, Last annotation update)
 DE Homeobox D8.
 GN Name=HOXD8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullany S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McKernan K.J., McKernan K.J., Gay L.J., Hulys S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski W.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; BC038709; AAH38709.1; -;
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeobox_in_like.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR DNA_BIND 195 254 Homeobox.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 289 AA; 31839 MW; 4C2621085174B447 CRC64;
 Query Match 54.9%; Score 45; DB 2; Length 289;
 Best Local Similarity 76.9%; Pred. No. 80;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12
 HXDE HUMAN STANDARD; PRT; 290 AA.
 AC P13378;
 DT 01-JUN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Homeobox protein Hox-d8 (Hox-4E) (Hox-5.4).
 GN Name=HoxD8; Synonym=HOXA4E;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Birren B., Linton L., Nusbaum C., Lander E.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
 RL "A complete mutation analysis panel of human HOX genes.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 193-287 FROM N.A.
 RX MEDLINE=89306602; PubMed=2568311;
 RA Oliver G., Sidel N., Fiske N., Heilmann C., Mohandas T.,
 RA Sparkes R.S., de Robertis E.M.,
 RL "Complementary homeo protein gradients in developing limb buds.";
 RL Genes Dev. 3:641-650(1989).
 CC -1- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the Antp homeobox family.
 CC -1- SIMILARITY: Contains 1 homeobox domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AC009336; -; NOT ANNOTATED_CDS.
 DR EMBL; AY014304; AAG42152.1; -
 DR EMBL; AY014303; AAG42152.1; JOINED.
 DR EMBL; X15507; CAA33529.1; -
 DR PIR; B32830; B32830.
 DR HSSP; P02833; 9ANT.
 DR TRASNFPAC; T03332; -
 DR Genew; HGNC:5139; HOXD8.
 DR MIM; 142985; -
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003700; F:transcription factor activity; NAS.
 DR GO; GO:0008555; P:determination of anterior/posterior axis, e...; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeodomain-like.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 15 23 Poly-Ala.
 FT DOMAIN 45 50 Poly-Ala.
 FT DOMAIN 109 123 Poly-Pro.

FT DNA BIND 197 256 Homeobox.
 FT CONFLICT 287 287 G -> A (in Ref. 3).
 SQ SEQUENCE 290 AA; 31910 MW; 75FF95A73E2A85F CRC64;
 Query Match 54.9%; Score 45; DB 1; Length 290;
 Best Local Similarity 76.9%; Pred. No. 80;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 YEAYKAAAAAPA 17
 DB 10 YSKYKAAAAAAA 22
 RESULT 13
 ID Q64CP3 PRELIMINARY; PRT; 707 AA.
 AC Q64CP3;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=GZ1D1_21;
 OS Uncultured archaean GZfos1D1.
 OC Archaea; environmental samples.
 OC NCBI_TaxID=286721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15353801;
 RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
 RA Richardson P.M., Delong E.F.;
 RL "Reverse methanogenesis: testing the hypothesis with environmental
 RL genomics.";
 RL Science 305:1457-1462(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY174833; AAU82834.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 707 AA; 78670 MW; 104F803EAS1973D CRC64;
 Query Match 54.9%; Score 45; DB 2; Length 707;
 Best Local Similarity 73.3%; Pred. No. 1.8e+02;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EKAYEAYKAAAAA 15
 DB 645 EKLSEAEARAAAAA 659
 RESULT 14
 ID Q82K16 PRELIMINARY; PRT; 949 AA.
 AC Q82K16;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=SAV2417;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OC NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RL "Genome sequence of an industrial microorganism Streptomyces
 RL avermitilis: deducing the ability of producing secondary
 RL metabolites.";

Search completed: February 26, 2005, 23:55:43
Job time : 75.898 secs

RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shida T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005030; BAC70128.1; -;
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR003781; COA binding.
DR InterPro; IPR000182; GCM5acetyl trans.
DR Pfam; PF00583; Acetyltransf_1; I.
DR Pfam; PF02629; COA_binding_1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 949 AA; 100557 MW; 98B8E5ED93FCC9D3 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 949;
Best Local Similarity 58.8%; Pred. No. 2,4e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYKRAAAAAAPA 17
Db 584 DQALAEALRSAAAAAPA 600

RESULT 15
Q9M3P6 PRELIMINARY; PRT; 71 AA.
AC Q9M3P6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Chitinase (fragment).
GN Name=CHI;
OS Hordeum marinum subsp. marinum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=112516;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21957723; PubMed=11962631; DOI=10.1139/g01-158;
RA De Bustos A., Loarce Y., Jouve N.;
RT "Species relationships between antifungal chitinase and nuclear rDNA
(internal transcribed spacer) sequences in the genus Hordeum.";
RL Genome 45:339-347(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400142; CAB7517.1; -;
DR HSSP; P23951; 2BAA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; I.
DR ProDom; PD354900; Glyco_hydro_19; I.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 7724 MW; SD6B896310B4C44C CRC64;

Query Match 53.7%; Score 44; DB 2; Length 71;
Best Local Similarity 64.3%; Pred. No. 31;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 KYEAYKRAAAAAAPA 17
Db 15 KYDAFLAAVAAPFA 28

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 / Search time 86.9082 Seconds
(without alignments)
75.654 Million cell updates/sec

Title: US-10-056-583A-97
Perfect score: 84
Sequence: 1 APEKAFKFAKAAAPA 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84	100.0	17	5	ABP52303	ABP52303 HLA-DR2 m
2	80	95.2	17	5	ABP52302	ABP52302 HLA-DR2 m
3	73	86.9	17	5	ABP52294	ABP52294 HLA-DR2 m
4	73	86.9	19	5	ABP52295	ABP52295 HLA-DR2 m
5	68	81.0	15	5	ABP52297	ABP52297 HLA-DR2 m
6	65	77.4	15	5	ABP52291	ABP52291 HLA-DR2 m
7	62	73.8	15	5	ABP52271	ABP52271 HLA-DR2 m
8	62	73.8	15	5	ABP52298	ABP52298 HLA-DR2 m
9	62	73.8	15	5	ABP52304	ABP52304 HLA-DR2 m
10	62	73.8	17	5	ABP52296	ABP52296 HLA-DR2 m
11	61	72.6	15	5	ABP52301	ABP52301 HLA-DR2 m
12	61	72.6	15	5	ABP52299	ABP52299 HLA-DR2 m
13	59	70.2	15	5	ABP52290	ABP52290 HLA-DR2 m
14	59	70.2	15	5	ABP52292	ABP52292 HLA-DR2 m
15	56	66.7	15	5	ABP52270	ABP52270 HLA-DR2 m
16	55	65.5	15	5	ABP52300	ABP52300 HLA-DR2 m
17	55	65.5	15	5	ABP52305	ABP52305 HLA-DR2 m
18	52	61.9	15	5	ABP52263	ABP52263 HLA-DR2 m
19	51	60.7	15	5	ABP52272	ABP52272 HLA-DR2 m
20	51	60.7	572	4	ABBS0072	ABBS0072 Drosophila
21	50	59.5	15	5	ABP52259	ABP52259 HLA-DR2 m
22	50	59.5	15	5	ABP52257	ABP52257 HLA-DR2 m
23	49	58.3	15	5	ABP52289	ABP52289 HLA-DR2 m
24	47	56.0	15	5	ABP52253	ABP52253 HLA-DR2 m
25	47	56.0	15	5	ABP52251	ABP52251 HLA-DR2 m

26	47	56.0	15	5	ABP52239	ABP52239 HLA-DR2 m
27	46	54.8	15	5	ABP52261	ABP52261 HLA-DR2 m
28	46	54.8	15	5	ABP52244	ABP52244 HLA-DR2 m
29	46	54.8	15	5	ABP52269	ABP52269 HLA-DR2 m
30	46	54.8	15	5	ABP52262	ABP52262 HLA-DR2 m
31	46	54.8	570	6	ADAS5549	ADAS5549 Human hea
32	46	54.8	570	7	ADJ70708	ADJ70708 Human hea
33	45	53.6	15	5	ABP52293	ABP52293 HLA-DR2 m
34	45	53.6	15	5	ABP52264	ABP52264 HLA-DR2 m
35	45	53.6	15	5	ABP52267	ABP52267 HLA-DR2 m
36	45	53.6	15	5	ABP52236	ABP52236 HLA-DR2 m
37	45	53.6	145	3	AAB32749	AAB32749 Eucalyptu
38	45	53.6	203	8	AD530243	AD530243 Bacterial
39	45	53.6	781	8	ADN60395	ADN60395 B. lichen
40	45	53.6	781	8	ADN60505	ADN60505 B. lichen
41	45	53.6	781	8	ADN60519	ADN60519 B. lichen
42	44	52.4	21	2	AAW19062	AAW19062 Trypanoso
43	44	52.4	21	2	AAW19087	AAW19087 Trypanoso
44	44	52.4	21	2	AAV32839	AAV32839 TCE repea
45	44	52.4	21	2	AAV33311	AAV33311 Epitope o

ALIGNMENTS

RESULT 1
ABP52303
ID ABP52303 standard; peptide; 17 AA.
XX
AC ABP52303;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KM immune response; antiinflammatory; neuroprotective; proliferation;
KM MHC class II protein inhibitor; demyelinating disease; inhibition;
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
KM anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 SQ Sequence 17 AA;
 XX
 XX
 Query Match 100.0%; Score 84; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APEKAKFEAYKAAAPA 17
 Db 1 APEKAKFEAYKAAAPA 17
 XX
 XX
 RESULT 2
 ID ABP52302 standard; peptide; 17 AA.
 XX
 XX ABP52302;
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
 XX
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 XX 24-JAN-2001; 2001US-0263569P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Strominger JL, Fridkis-Hareli M;
 PI
 DR WPI; 2002-608439/65.
 XX
 XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 PT
 XX
 XX Claim 28; Page 39; 54pp; English.
 PS
 XX The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX

SQ Sequence 17 AA;
 XX
 XX
 Query Match 95.2%; Score 80; DB 5; Length 17;
 Best Local Similarity 94.1%; Pred. No. 4.2e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APEKAKFEAYKAAAPA 17
 Db 1 APEKAKFEAYKAAAPA 17
 XX
 XX
 RESULT 3
 ID ABP52294 standard; peptide; 17 AA.
 XX
 XX ABP52294;
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
 XX
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 XX 24-JAN-2001; 2001US-0263569P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Strominger JL, Fridkis-Hareli M;
 PI
 DR WPI; 2002-608439/65.
 XX
 XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 PT
 XX
 XX Claim 28; Page 39; 54pp; English.
 PS
 XX The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 SQ Sequence 17 AA;
 XX
 XX
 Query Match 86.9%; Score 73; DB 5; Length 17;
 Best Local Similarity 88.2%; Pred. No. 5.9e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APEKAKFEAYKAAAPA 17

KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX WPI; 2002-608439/65.
 DR
 PS
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
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 PS Claim 28; Page 39; 54pp; English.
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 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP5305 represent peptides used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 77.4%; Score 65; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0011;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EKAKFEAYKAAAPA 17
 DB 1 EKPKYEAYKAAAPA 15
 ID ABP52271 standard; peptide; 15 AA.
 AC ABP52271;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX

OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX WPI; 2002-608439/65.
 DR
 PS
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP5305 represent peptides used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 73.8%; Score 62; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0033;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EKAKFEAYKAAAPA 17
 DB 1 EKAKYEAYKAAAPA 15
 ID ABP52298 standard; peptide; 15 AA.
 AC ABP52298;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX

PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 73.8%; Score 62; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0033;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EKAKFEAYKAAAPAA 17
 | | | | | | | | | | | | | | | | |
 1 EKAKFEAYKAAAPAA 15
 Db
 RESULT 9
 ABP52304
 ID ABP52304 standard; peptide; 15 AA.
 XX
 AC ABP52304;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:98.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA Strominger JL, Fridkis-Hareli M;
 XX
 PI

XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
 XX
 CC The present invention describes compositions (I) comprising a peptide
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 73.8%; Score 62; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0033;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 EKAKFEAYKAAAPAA 17
 | | | | | | | | | | | | | | | | |
 1 EKAKFEAYKAAAPAA 15
 Db
 RESULT 10
 ABP52296
 ID ABP52296 standard; peptide; 17 AA.
 XX
 AC ABP52296;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
 XX
 KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KM immune response; antiinflammatory; neuroprotective; proliferation;
 KM MHC class II protein inhibitor; demyelinating disease; inhibition;
 KM post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KM anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

CC ABP52305 represent peptides used in the exemplification of the present invention

XX Sequence 15 AA;

Query Match 72.6%; Score 61; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0048;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPA 17
DB 1 EKPRYEAYKAAAPA 15

RESULT 13

ABP52290 standard; peptide; 15 AA.

ID ABP52290 standard; peptide; 15 AA.

XX ABP52290;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:84.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

OS Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 15 AA;

Query Match 70.2%; Score 59; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.01;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPA 17
DB 1 EKPRYEAYKAAAPA 15

RESULT 14

ABP52292 standard; peptide; 15 AA.

ID ABP52292 standard; peptide; 15 AA.

XX ABP52292;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:86.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

OS Homo sapiens.
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
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CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
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CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention

XX Sequence 15 AA;

Query Match 70.2%; Score 59; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.01;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPA 17
DB 1 EKPRYEAYKAAAPA 15

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RESULT 15
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX AC
XX ABP52270;
XX DT
XX 16-OCT-2002 (first entry)
XX DE
XX HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX immune response; antiinflammatory; neuroprotective; proliferation;
XX MHC class II protein inhibitor; demyelinating disease; inhibition;
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX WO200259143-A2.
XX PN
XX 01-AUG-2002.
XX PD
XX 24-JAN-2002; 2002WO-US002071.
XX PF
XX 24-JAN-2001; 2001US-0263569P.
XX PR
XX (HARD ) HARVARD COLLEGE.
XX PA
XX Strominger JL, Fridkis-Hareli M;
XX FI
XX WPI; 2002-608439/65.
XX DR
XX
XX New compositions comprising synthetic peptides in complex with a major
XX PT histocompatibility class II HLA-DR2 protein, useful for treating a
XX PT demyelinating disease, e.g. multiple sclerosis, or post-viral
XX PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX PS
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XX The present invention describes compositions (I) comprising a peptide
XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX CC residues. The complex of the peptide with a major histocompatibility
XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX CC immune response. (I) has antiinflammatory and neuroprotective activities,
XX CC and can be used as a MHC class II protein inhibitor. The compositions
XX CC comprising the peptides are useful for treating demyelinating diseases
XX CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
XX CC demyelinating condition, and a side effect of administering an anti-
XX CC tumour necrosis factor agents. The peptide further inhibits proliferation
XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
XX CC ABP52305 represent peptides used in the exemplification of the present
XX CC invention
XX
XX Sequence 15' AA:
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Query Match 66.7%; Score 56; DB 5; Length 15;
 Best Local Similarity 80.0%; Pred. No. 0.031;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 3 EKAKFEAYKAAAPA 17
   | | | | | | | | | |
Db 1 EAAKTEAYKAAAPA 15

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Search completed: February 26, 2005, 23:48:25
 Job time : 87.9082 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 22.7245 Seconds
(Without alignments)
55.844 Million cell updates/sec

Title: US-10-056-583a-97

Perfect score: 84

Sequence: 1 APEKAFKFAVKAAPAA 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	45	53.6	212	4	US-09-902-540-16451
3	44	52.4	21	2	US-08-557-3098-58
4	44	52.4	21	2	US-08-929-414-11
5	44	52.4	21	3	US-08-834-306-56
6	44	52.4	21	3	US-08-834-306-56
7	44	52.4	21	3	US-08-993-674A-56
8	44	52.4	21	3	US-08-993-674A-56
9	44	52.4	21	4	US-09-256-976-56
10	44	52.4	21	4	US-09-256-976-56
11	44	52.4	262	1	US-08-403-379A-1
12	44	52.4	262	2	US-08-929-414-1
13	44	52.4	262	2	US-08-557-3098-51
14	44	52.4	263	3	US-08-834-306-51
15	44	52.4	263	3	US-08-993-674A-51
16	44	52.4	263	4	US-08-993-674A-51
17	43	51.2	469	4	US-09-256-976-51
18	43	51.2	639	4	US-09-252-991A-27869
19	43	51.0	639	4	US-09-854-791A-17
20	42	50.2	324	4	US-09-248-796A-1756
21	41	48.8	21	2	US-08-557-3098-61
22	41	48.8	21	2	US-08-929-414-13
23	41	48.8	21	3	US-08-834-306-60
24	41	48.8	21	3	US-08-993-674A-60
25	41	48.8	21	3	US-09-256-976-60
26	41	48.8	245	3	US-08-486-099-104
27	41	48.8	245	3	US-08-360-107A-114

28	41	48.8	245	3	US-08-484-223B-104	Sequence 104, App
29	41	48.8	245	3	US-08-919-597-104	Sequence 104, App
30	41	48.8	245	3	US-08-475-668A-104	Sequence 104, App
31	41	48.8	245	3	US-08-485-551A-104	Sequence 104, App
32	41	48.8	245	3	US-08-471-913A-104	Sequence 104, App
33	41	48.8	245	3	US-08-485-264A-104	Sequence 104, App
34	41	48.8	245	3	US-08-474-349A-104	Sequence 104, App
35	41	48.8	245	3	US-08-470-896-104	Sequence 104, App
36	41	48.8	245	4	US-08-485-546A-104	Sequence 104, App
37	41	48.8	245	4	US-08-487-266A-104	Sequence 104, App
38	41	48.8	246	4	US-09-350-841A-1590	Sequence 1590, App
39	41	48.8	642	4	US-09-489-039A-12434	Sequence 12434, A
40	41	48.8	1020	4	US-09-538-092-911	Sequence 911, App
41	40.5	48.2	68	4	US-09-540-236-3324	Sequence 3324, App
42	40	47.6	21	1	US-08-403-379A-3	Sequence 3, App1
43	40	47.6	21	1	US-08-557-3098-52	Sequence 52, App1
44	40	47.6	21	2	US-08-557-3098-57	Sequence 57, App1
45	40	47.6	21	2	US-08-557-3098-60	Sequence 60, App1

ALIGNMENTS

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RESULT 1
US-09-640-211A-798
; Sequence 798, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-798

Query Match      53.6%; Score 45; DB 4; Length 145;
Best Local Similarity 64.7%; Pred. No. 3.8;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 APEKAFKFAVKAAPAA 17
Db      113 APEKAFKFAVKAAPAA 129

RESULT 2
US-09-902-540-16451
; Sequence 16451, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16451
; LENGTH: 212
; TYPE: PRT

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ORGANISM: Myxococcus xanthus
US-09-902-540-16451

Query Match 53.6%; Score 45; DB 4; Length 212;
Best Local Similarity 60.0%; Pred. No. 5.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEKAKFEAYKAAAP 16
DB 134 PDQAPFDALIAAP 148

RESULT 3
US-08-557-309B-58
Sequence 58, Application US/08557309B
Patent No. 5915572

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-557-309B-58

Query Match 52.4%; Score 44; DB 2; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKAYKAAAP 17
DB 5 APAKAAAPAKAAAP 21

RESULT 4
US-08-929-414-11
Sequence 11, Application US/08929414
Patent No. 5942403

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Haughton, Raymond
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION
OF T. CRUZI INFECTION

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,414
FILING DATE: 15-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-929-414-11

Query Match 52.4%; Score 44; DB 2; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFKAYKAAAP 17
DB 5 APAKAAAPAKAAAP 21

RESULT 5
US-08-834-306-56
Sequence 56, Application US/08834306
Patent No. 6054135

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-834-306-56

Query Match 52.4%; Score 44; DB 3; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17
Db 5 APAKAAAPAKAAAPA 21

RESULT 6
US-08-834-306-58
Sequence 58, Application US/08834306
Patent No. 6054135
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-834-306-58

Query Match 52.4%; Score 44; DB 3; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17
Db 5 APAKAAAPAKAAAPA 21

RESULT 7
US-08-993-674A-56
Sequence 56, Application US/08993674A

Patent No. 6228372
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-674A-56

Query Match 52.4%; Score 44; DB 3; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17
Db 5 APAKAAAPAKAAAPA 21

RESULT 8
US-08-993-674A-58
Sequence 58, Application US/08993674A
Patent No. 6228372
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,674A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-993-674A-58
;
Query Match          52.4%; Score 44; DB 3; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPAA 17
   ||| ||| ||| ||| |||
Db 5 APAKAAAAAPAKAAAPAA 21

RESULT 9
US-09-256-976-56
; Sequence 56, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
; TITLE OF INVENTION: OF T. CRUZI INFECTION
; FILE REFERENCE: 210121.422C3
; CURRENT APPLICATION NUMBER: US/09/256,976
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TCE antigenic
; OTHER INFORMATION: epitope
US-09-256-976-56:
;
Query Match          52.4%; Score 44; DB 4; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPAA 17
   ||| ||| ||| ||| |||
Db 5 APAKAAAAAPAKAAAPAA 21

RESULT 10
US-09-256-976-58
; Sequence 58, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
```

```

; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
; TITLE OF INVENTION: OF T. CRUZI INFECTION
; FILE REFERENCE: 210121.422C3
; CURRENT APPLICATION NUMBER: US/09/256,976
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TCE
; OTHER INFORMATION: antigenic epitope
US-09-256-976-58
;
Query Match          52.4%; Score 44; DB 4; Length 21;
Best Local Similarity 64.7%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPAA 17
   ||| ||| ||| ||| |||
Db 5 APAKAAAAAPAKAAAPAA 21
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RESULT 11
US-08-403-379A-1
; Sequence 1, Application US/08403379A
; Patent No. 5756662
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION
; TITLE OF INVENTION: OF T. CRUZI INFECTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,379A
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-379A-1
;
Query Match          52.4%; Score 44; DB 1; Length 262;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 1 APEKAKFEAYKAAAPAA 17
Db 141 AAAAAAAAAAAAAAAAAA 157

RESULT 12

US-08-929-414-1
Sequence 1, Application US/08929414
Patent No. 5942403

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION
OF T. CRUZI INFECTION
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,414
FILING DATE: 15-SEP-1997

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.
REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.406C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-929-414-1

Query Match 52.4%; Score 44; DB 2; Length 262;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPAA 17
Db 141 AAAAAAAAAAAAAAAAAA 157

RESULT 13

US-08-557-309B-51
Sequence 51, Application US/08557309B
Patent No. 5916572

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
PREVENTION OF T
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98104-7092
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-557-309B-51

Query Match 52.4%; Score 44; DB 2; Length 263;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPAA 17
Db 142 AAAAAAAAAAAAAAAAAA 158

RESULT 14

US-08-834-306-51
Sequence 51, Application US/08834306
Patent No. 6054135

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
PREVENTION OF T
NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
US-08-834-306-51

Query Match 52.4%; Score 44; DB 3; Length 263;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAEAYKAAAPA 17
DB 142 APAKAAAPAKAAAPA 158

RESULT 15

US-08-993-674A-51
Sequence 51, Application US/08993674A
Patent No. 6228372
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-993-674A-51

Query Match 52.4%; Score 44; DB 3; Length 263;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAEAYKAAAPA 17
DB 142 APAKAAAPAKAAAPA 158

Search completed: February 26, 2005, 23:59:31
Job time : 23.7245 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 60.7143 Seconds
(without alignments)
91.852 Million cell updates/sec

Title: US-10-056-583A-97

Perfect score: 84

Sequence: 1 APEKAKEAYKAAAPA 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10E_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	17	US-10-056-583-97	Sequence 97, Appl
2	80	95.2	17	US-10-056-583-96	Sequence 96, Appl
3	73	86.9	17	US-10-056-583-88	Sequence 88, Appl
4	73	86.9	19	US-10-056-583-89	Sequence 89, Appl
5	68	81.0	15	US-10-056-583-91	Sequence 91, Appl
6	65	77.4	15	US-10-056-583-85	Sequence 85, Appl
7	62	73.8	15	US-10-056-583-65	Sequence 65, Appl
8	62	73.8	15	US-10-056-583-98	Sequence 98, Appl
9	62	73.8	17	US-10-056-583-90	Sequence 90, Appl
10	61	72.6	15	US-10-056-583-93	Sequence 93, Appl
11	61	72.6	15	US-10-056-583-95	Sequence 95, Appl
12	59	70.2	15	US-10-056-583-84	Sequence 84, Appl
13	59	70.2	15	US-10-056-583-86	Sequence 86, Appl

14	56	66.7	15	US-10-056-583-64	Sequence 64, Appl
15	56	66.7	15	US-10-056-583-92	Sequence 92, Appl
16	55	65.5	15	US-10-056-583-94	Sequence 94, Appl
17	55	65.5	15	US-10-056-583-99	Sequence 99, Appl
18	52	61.9	15	US-10-056-583-57	Sequence 57, Appl
19	51	60.7	15	US-10-056-583-66	Sequence 66, Appl
20	50	59.5	15	US-10-056-583-51	Sequence 51, Appl
21	50	59.5	15	US-10-056-583-53	Sequence 53, Appl
22	49	58.3	15	US-10-056-583-83	Sequence 83, Appl
23	47	56.0	15	US-10-056-583-33	Sequence 33, Appl
24	47	56.0	15	US-10-056-583-45	Sequence 45, Appl
25	46	54.8	15	US-10-056-583-47	Sequence 47, Appl
26	46	54.8	15	US-10-056-583-38	Sequence 38, Appl
27	46	54.8	15	US-10-056-583-55	Sequence 55, Appl
28	46	54.8	15	US-10-056-583-56	Sequence 56, Appl
29	46	54.8	15	US-10-056-583-63	Sequence 63, Appl
30	46	54.8	15	US-10-094-749-3117	Sequence 3117, Ap
31	46	54.8	15	US-10-408-765A-2514	Sequence 2514, Ap
32	45	53.6	15	US-10-056-583-30	Sequence 30, Appl
33	45	53.6	15	US-10-056-583-58	Sequence 58, Appl
34	45	53.6	15	US-10-056-583-61	Sequence 61, Appl
35	45	53.6	15	US-10-056-583-87	Sequence 87, Appl
36	45	53.6	203	US-10-369-493-19276	Sequence 19276, A
37	45	53.6	265	US-10-424-599-180279	Sequence 180279, A
38	45	53.6	265	US-10-425-114-54748	Sequence 54748, A
39	43	51.2	15	US-10-056-583-59	Sequence 59, Appl
40	43	51.2	180	US-10-424-599-266399	Sequence 266399, A
41	43	51.2	267	US-10-437-963-134556	Sequence 134556, A
42	43	51.2	386	US-10-437-963-194029	Sequence 194029, A
43	43	51.2	404	US-10-437-963-134562	Sequence 134562, A
44	43	51.2	421	US-10-282-122A-56483	Sequence 56483, A
45	43	51.2	465	US-10-282-122A-66168	Sequence 66168, A

ALIGNMENTS

RESULT 1
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: President and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMENTIA
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match 100.0%; Score 84; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKEAYKAAAPA 17
|||||
Db 1 APEKAKEAYKAAAPA 17

RESULT 2
US-10-056-583-96

Sequence 96, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Harell, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 96
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-96

Query Match	95.2%	Score 80;	DB 14;	Length 17;
Best Local Similarity	94.1%	Pred. No. 1.8e-06;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```
Qy      1 APEKAKEEAYKAAAAPA 17
         |||||:|||||
Db      1 APEKAKEEAFKAAAAPA 17
```

```

RESULT 3
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DENEYLINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24695-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
; US-10-056-583-88

```

Query Match	86.9%	Score 73	DB 14	Length 17
Best Local Similarity	88.2%	Pred. No. 2.6e-05		
Matches	15	Conservative	1	Mismatches 1, Indels 0, Gaps 0
Qy	1	APEKAKFEAYVQALAAFA	17	
Db	1	APEKAKFEAYVRAAAAAA	17	

RESULT 4
US-10-056-583-89
; Sequence 89, Application US/100556583
; Publication NO. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.

```

1  APPLICANT: Fridkis-Harell, Masha
2  TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
3  TITLE OF INVENTION: CONDITIONS
4  FILE REFERENCE: 24655-017
5  CURRENT APPLICATION NUMBER: US/10/056,583
6  CURRENT FILING DATE: 2002-01-24
7  PRIOR APPLICATION NUMBER: 60/263,569
8  PRIOR FILING DATE: 2001-01-24
9  NUMBER OF SEQ ID NOS: 99
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO 89
12 LENGTH: 19
13 TYPE: PRT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: The peptide was designed and synthesized
17 US-10-056-583-89

```

Query Match	86.9%;	Score 73;	DB 14;	Length 19;
Best Local Similarity	88.2%;	Pred. No. 2.9e-05;		
Matches 15; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

```
Qy      1 APEKAKFEAYKAAAPA 17
         |||||:|||||||
Db      1 APEKAKFEAYKAAAAA 17
```

```

RESULT 5
US-10-056-583-91
; Sequence 91, Application US/100556583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
; US-10-056-583-91

```

Query Match	81.0%	Score 68;	DB 14;	Length 15;
Best Local Similarity	93.3%	Pred. No. 0.00015;		
Matches 14; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	3	EKAKFEAYKAAAP	17
Db	1	EKPKEAYKAAAP	15

RESULT 6
US-10-056-583
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridakis-Harell, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056, 583

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
```

```
Query Match          77.4%; Score 65; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          3 EKAKFEAYKAAAPAA 17
|||:|||||
Db          1 EKPKYEAYKAAAPAA 15
```

```
RESULT 7
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match          73.8%; Score 62; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          3 EKAKFEAYKAAAPAA 17
|||:|||||
Db          1 EKAKYEAYKAAAPAA 15
```

```
RESULT 8
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98
```

```
Query Match          73.8%; Score 62; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          3 EKAKFEAYKAAAPAA 17
|||:|||||
Db          1 EAPKFEAYKAAAPAA 15
```

```
RESULT 9
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match          73.8%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY          3 EKAKFEAYKAAAPAA 17
|||:|||||
Db          1 EKAKYEAYKAAAPAA 15
```

```
RESULT 10
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93

Query Match 72.6%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17
| | | | | | | | | | | | | | | | |
Db 1 EKPKVEAYKAAAPAA 15

RESULT 11
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match 72.6%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17
| | | | | | | | | | | | | | | | |
Db 1 EKAKFEAYKAAAPAA 15

RESULT 12
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match 70.2%; Score 59; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0048;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17
| | | | | | | | | | | | | | | | |
Db 1 EAPKVEAYKAAAPAA 15

RESULT 13
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match 70.2%; Score 59; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0048;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17
| | | | | | | | | | | | | | | | |
Db 1 EAPKVEAYKAAAPAA 15

RESULT 14
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

Query Match 66.7%; Score 56; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.015;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17
| | | | | | | | | | | | | | | | |
Db 1 EAAKFEAYKAAAPAA 15

RESULT 15

US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match 66.7%; Score 56; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. NO. 0.015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 EKAKFEAYKAAAPAA 17
Db 1 EKAKFEAYKAAAPAA 15

Search completed: February 27, 2005, 00:05:24
Job time : 61.7143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 15.0918 Seconds
(without alignments)
108.382 Million cell updates/sec

Title: US-10-056-583A-97

Perfect score: 84

Sequence: 1 APEKAKEAYKAAAPA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	54.8	179	2	F97683
2	46	54.8	179	2	AF2908
3	45	53.6	389	2	G87332
4	45	53.6	408	2	AH3269
5	44	52.4	73	2	S40015
6	44	52.4	97	2	S60110
7	43	51.2	421	2	JV0057
8	43	51.2	465	2	D83598
9	43	51.2	639	1	T02784
10	42.5	50.6	189	2	S77930
11	42.5	50.6	189	2	S77935
12	42	50.0	84	2	T23177
13	42	50.0	88	2	JC2184
14	42	50.0	405	2	AH2752
15	42	50.0	457	2	F97533
16	42	50.0	1612	2	JC5210
17	42	50.0	2113	2	G91286
18	42	50.0	2113	2	C86128
19	41	48.8	200	1	Q0B827
20	41	48.8	447	2	AB3359
21	41	48.8	629	2	AH0521
22	41	48.8	1020	1	QFNUH
23	40	47.6	128	2	T40464
24	40	47.6	151	1	HSMT2A
25	40	47.6	168	2	A45943
26	40	47.6	184	2	D83234
27	40	47.6	265	2	A87193
28	40	47.6	416	2	AB1609
29	40	47.6	565	2	C87278

30	40	47.6	591	2	T39726	probable lysyl-tn
31	40	47.6	641	2	PH1919	Fr-160-4 protein -
32	40	47.6	829	2	E64114	translation initia
33	40	47.6	1132	2	C75259	probable iron-sulf
34	39.5	47.0	68	2	EX0019	phospholipase A2 (
35	39	46.4	106	2	AB1203	conserved hypochet
36	39	46.4	117	2	C81779	hypothetical prote
37	39	46.4	129	1	TNLJG3	trans-activating t
38	39	46.4	137	2	PO0065	T-cell receptor be
39	39	46.4	159	2	A97836	hypothetical prote
40	39	46.4	162	2	H70927	probable rps8 prot
41	39	46.4	165	2	B87702	ribosomal protein
42	39	46.4	185	2	S36290	T-cell receptor ga
43	39	46.4	202	2	A83492	probable transcrip
44	39	46.4	321	2	T07932	probable 1-aminocy
45	39	46.4	327	2	A56553	homeotic protein H

ALIGNMENTS

RESULT 1

F97683 50S ribosomal protein l19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C/Accession: F97683

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lepas, C.; Markelz, B.

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: F97683

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-179 <KUR>

A/Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AXX88423.1; PID:G15157917; GSPDB:

C/Genetics:

A/Gene: AGR_C_4900

A/Map position: circular chromosome

C/Superfamily: Escherichia coli ribosomal protein l19

Query Match 54.8%; Score 46; DB 2; Length 179;

Best Local Similarity 64.7%; Pred. No. 3.1;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAKEAYKAAAPA 17

Db 135 ABEKARLEKVAQAQ 151

RESULT 2

AF2908 50S ribosomal protein l19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AF2908

R/Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AF2908

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-179 <KUR>

A/Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAI43684.1; PID:G17741210; GSPDB:

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: rps15

A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match	54.8%;	Score 46;	DB 2;	Length 179;
Best Local Similarity	64.7%;	Pred. No. 3.1;		
Matches 11; Conservative	1;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      1 APEKAKFEAYKAAAPAP 17
          | | | : | | | | |
Db      135 AEEKARLEAEKVAAPQA 151
```

RESULT 3
G87332
hypothetical protein CC0674 [imported] - *Caulobacter crescentus*
hypothetical protein CC0674 [imported] - *Caulobacter crescentus*

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: G67332
R:NIEMAN, W.C.; FELDLHYM, T.V.; PAULSEN, I.T.; NELSON, K.E.; EISEN, J.; HEIDELBERG, J.
B.; LABB, M.T.; DEBOY, R.T.; DODSON, R.J.; DURKIN, A.S.; GWINN, M.L.; HATT, D.H.; KOLON
N, J.; ERMOLEVA, M.; WHITE, O.; SALZBERG, S.L.; SHAPIRO, L.; VENTER, J.C.; FRASER, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A67249; MUID:21173698; PMID:11259647

Query Match	53.6%	Score 45;	DB 2;	Length 389;
Best Local Similarity	58.8%;	Pred. No. 9.6;		
Matches 10;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;

```
QY      1 APEKAKFEAYKAAAAAPA 17
          | | | | | | | |
Db      63 ADGKTSVETFKAAAAAPA 79
```

RESULT 4
AH3269
dihydrodipamide-S-succinyltransferase (EC 2.3.1.61) [imported] - *Brucella melitensis* (6
C/Species: *Brucella melitensis*
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

R; DelVecchio, V.G.; Kapatrail, V.; Redkar, R.U.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, P. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

Article: The genome sequence of the facultative intracellular pathogen *Brucella melitensis* A; Reference number: AD3252; PMID:11756688

A;Status: preliminary
A;Molecule type:: DNA
A;Residues: 1-408 <KUR>
A;Cross-references: UNIPROT:Q9J6H8; GB:AE008917; PIDD:AL5133.1; PIDD:g17982020; GSFDB:G000000000
A;Experimental source: strain 16M

Query Match	53.6%	Score 45;	DB 2;	Length 408;
Best Local Similarity	64.7%;	Pred. No. 10;		
Matches 11;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      1 APEKAKFEAYKAAAAPA 17
        . || : || || || || ||
Db      86 APAQKKEEAKPAAAAAPA 102
```

RESULT 5
S4015
pnd protein - phage P1

C.Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C.Accession: S40015, S38553
C.Lehner, H.; Maguin, E.; Jafari, S.; Yarmolinsky, M. B.
J. Mol. Biol. 233, 414-428, 1993
A.Title: Plasmid addiction of bacteriophage P1: doc, which causes cell death on cure
A.Reference numbers: S40015, MUID:9401561; PMID:8411153

A: Molecule type: DNA
A: Residues: 1-73 <LEF>
A: Cross-references: UNIPROT: Q06253; GB: M05666; NID: g463276; PIDN: AAA16932.1; PID: g215644
R: Schmidt, C., Lemmer, H., Guddolin, A., Arbes, W.
submitted to the EMBL Data Library, November 1992
A: Description: Additional late promoter sequences of bacteriophage P1.
A: Reference number: 538553

Query Match	52.4%	Score 44;	DB 2;	Length 73;
Best Local Similarity	71.4%;	Pred. No. 2.7;		
Matches 10; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      4 KAKFEAYKAAAP 17
         |||||
Db      41 KATFEAYKKAALDA 54
```

RESULT 6
G60110
repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)
C1Species: Trypanosoma cruzi

C;Accession: G60110
R;Host, D.F.; Kim, K.S.; Oteu, K.; Moser, D.R.; Yost, W.J.; Blumkin, J.H.; Donelson, J.E
Infect. Immun. 57, 1959-1967, 1989
A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A;Reference number: A60110; MUID:89277508; PMID:2659529

A:Cross-references: UNIPROT:Q7M3M1
C:Superfamily: varicella-zoster virus gene 22 protein
C:Keywords: tandem repeat
F:1-85/Region: 7-residue repeats

QY	1	APEKAKEAYKAAAPA	17
Db	2	APAKAAAAAPAKAAAA	18

RESULT 7,
JV0057
cola protein - Escherichia coli (strain K-12)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Defn: *Escherichia coli* O157:H7
 C:Accession: J00057; B64810
 C:Levensgood, S.K.; Webster, R.E.
 J. Bacteriol. 171, 6600-6609, 1989
 A:Title: Nucleotide sequences of the *tolA* and *tolB* genes and localization of their products
 R:Reference number: J00057; MUID:90078104; PMID:267247

```

A:Reference number: Z14736
A:Accession: T02784
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-639 <MOR>
A:Cross-references: UNIPROT:O82107; EMBL:AJ007366; PIDD:CAA07481.1
A:Experimental source: strain W64A; seed
C:Function:
C:Description: probably involved in pathogen defense in maize plants
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F:151-411/Domain: protein kinase homology <KIN>
F:159-167/Region: protein kinase ATP-binding motif
F:454-486/Domain: calmodulin repeat homology <EF1>
F:490-522/Domain: calmodulin repeat homology <EF2>
F:526-558/Domain: calmodulin repeat homology <EF3>
F:560-592/Domain: calmodulin repeat homology <EF4>
F:182/Active site: Lys #status predicted

Query Match          51.2%; Score 43; DB 1; Length 639;
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Cy 1 APEKAKFEAYKAAAPA 17
    ||| | | | | | |
Db 68 APEPVKTAAYHSEPPA 84

RESULT 10
exoskeletal protein HACP202A - American lobster (fragment)
C:Species: Homarus americanus (American lobster)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S77930
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
Submitted to the Protein Sequence Database, June 1997
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus
A:Reference number: S77925
A:Accession: S77930
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-189 <NOU>
A:Cross-references: UNIPROT:Q7M496

Query Match          50.6%; Score 42.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Cy 1 APEKAK-PEAYKAAAPA 17
    ||| | | | | | |
Db 9 AAEKARFFOAKAEAAA 26

RESULT 11
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C:Species: Homarus americanus (American lobster)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S77935
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
Submitted to the Protein Sequence Database, June 1997
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus
A:Reference number: S77925
A:Accession: S77935
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-189 <NOU>
A:Cross-references: UNIPROT:Q7M495

Query Match          50.6%; Score 42.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

```

OY 1 APEKAKFEAYKAAAPA 17
 |||||
 Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 12

T23177
 hypothetical protein K01D12.7 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T23177, T23188
 R/Johnson, R.
 Submitted to the EMBL Data Library, June 1996
 A/Reference number: Z19703
 A/Accession: T23177
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-84 <MTL>
 A/Cross-references: UNIPROT:Q27223; UNIPROT:Q95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB:
 A/Experimental source: clone K01D12
 A/Accession: T23188
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-84 <MT2>
 A/Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CESP:K01D12.15
 A/Experimental source: clone K01D12
 C/Genetics:
 A/Gene: CESP:K01D12.7; CESP:K01D12.15
 A/Map position: 5

Query Match 50.0%; Score 42; DB 2; Length 84;
 Best Local Similarity 62.5%; Pred. No. 6.7;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 2 PEKAKFEAYKAAAPA 17
 |||||
 Db 34 PPKASATKKAAPPA 49

RESULT 13

JC2184
 transcription factor Brn-3R - mouse (fragment)
 C/Species: *Mus musculus* (house mouse)
 C/Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 16-Aug-2004
 C/Accession: JC2184, S41455
 R/John, B.; Chicaiza, G.; Martin, F.; Jaggi, R.
 Biochem. Biophys. Res. Commun. 200, 156-162, 1994
 A/Title: Isolation of three novel POU-domain containing cDNA clones from lactating mouse
 A/Reference number: JC2182; MUID:94220079; PMID:816682
 A/Accession: JC2184
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-88 <JEH>
 A/Cross-references: UNIPROT:Q62091; EMBL:Z29629
 A/Experimental source: mammary gland
 R/John, B.; Chicaiza, G.; Martin, F.; Jaggi, R.
 Submitted to the EMBL Data Library, January 1994
 A/Description: Isolation of three novel POU-domain containing cDNA clones from lactating
 A/Reference number: S41454
 A/Accession: S41455
 A/Molecule type: mRNA
 A/Residues: 1-45, 'F', 47-88 <JE2>
 A/Cross-references: EMBL:Z29629; MUID:9452415; PIDN:CAA82736.1; PID:9452416
 C/Suprafamily: homeobox homology; POU domain homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F.1-33/Domain: POU domain homology (fragment) <POU>
 F.49-88/Domain: homeobox homology (fragment) <HOX>

Query Match 50.0%; Score 42; DB 2; Length 88;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 APEKAKFEAYKAA 12

Db 59 APEKASLEAYFA 70
 |||||

RESULT 14

AH2752
 dihydroliipoamide acetyltransferase [imported] - *Agrobacterium tumefaciens* (strain C58, D
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C/Accession: AH2752
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tso, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AH2752
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-405 <KUR>
 A/Cross-references: UNIPROT:Q8URF5; GB:AE008688; PIDN:AAL42438.1; PID:gl7739851; GSPDB:C
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Gene: acef
 A/Map position: circular chromosome

Query Match 50.0%; Score 42; DB 2; Length 405;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 2 PEKAKFEAYKAAAP 16
 |||||
 Db 56 PEAKAKAPKEEAP 70

RESULT 15

F97533
 dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (e2) [imp
 C/Species: *Agrobacterium tumefaciens*
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: F97533
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.,
 Science 284, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: F97533
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-457 <KUR>
 A/Cross-references: UNIPROT:Q8URF5; GB:AE007869; PIDN:AAK87223.1; PID:gl5156505; GSPDB:C
 A/Experimental source: circular chromosome
 A/Gene: AGR_C_2641
 C/Suprafamily: dihydroliipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 50.0%; Score 42; DB 2; Length 457;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 2 PEKAKFEAYKAAAP 16
 |||||
 Db 108 PEAKAKAPKEEAP 122

Search completed: February 26, 2005, 23:57:18
 Job time : 16.0918 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 73.898 Seconds
(without alignments)
117.802 Million cell updates/sec

Title: US-10-056-583a-97
Perfect score: 84
Sequence: 1 APEKAKFEAYKAAAPA 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnlProt_03:*
1: unlprot_sprot:*
2: unlprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	60.7	574	2 Q8SXM8	Q8SXM8 dtrosophila
2	51	60.7	607	2 Q9W327	Q9W327 dtrosophila
3	46	54.8	179	1 RL9 AGRT5	Q9W327 agrobacteri
4	46	54.8	570	2 Q9W327	Q9W327 agrobacteri
5	45	53.6	183	2 Q81W24	Q81W24 bacillus an
6	45	53.6	244	2 Q8JHA3	Q8JHA3 gallus gall
7	45	53.6	389	2 Q9AAC8	Q9AAC8 caulobacter
8	45	53.6	390	2 Q85598	Q85598 bruceella ab
9	45	53.6	408	2 Q8FVR8	Q8FVR8 bruceella su
10	45	53.6	408	2 Q9L6H8	Q9L6H8 bruceella me
11	45	53.6	607	2 Q8PGF8	Q8PGF8 xanthomonas
12	45	53.6	781	2 Q65JG3	Q65JG3 bacillus li
13	45	53.6	1340	2 Q69YQ8	Q69YQ8 homo sapien
14	45	53.6	1614	2 Q69YQ9	Q69YQ9 homo sapien
15	44.5	53.0	427	2 Q98BE9	Q98BE9 rhizobium l
16	44	52.4	73	1 PHD_BPP1	PHD_BPP1
17	44	52.4	73	2 Q79A04	Q79A04 bacterioph
18	44	52.4	87	2 Q8TJG9	Q8TJG9 escherichia
19	44	52.4	97	2 Q7M3W1	Q7M3W1 methanosarc
20	44	52.4	272	2 Q8P7P0	Q8P7P0 trypanosom
21	44	52.4	2034	2 Q872S0	Q872S0 xanthomonas
22	43.5	51.8	306	2 Q7XJ55	Q7XJ55 neurospora
23	43	51.2	153	2 Q7XVTS	Q7XVTS oryza sativ
24	43	51.2	163	2 Q6JRS4	Q6JRS4 equus cabal
25	43	51.2	174	2 Q73FJ2	Q73FJ2 bacillus ce
26	43	51.2	177	1 RL9 RHIME	RL9 RHIME
27	43	51.2	181	1 RL9 RHIL0	RL9 RHIL0
28	43	51.2	190	2 Q6AH83	Q6AH83 rhizobium l
29	43	51.2	238	2 Q62WL2	Q62WL2 leifsonia x
30	43	51.2	240	2 Q65L73	Q65L73 bacillus li
31	43	51.2	404	2 Q7F9Q4	Q7F9Q4 oryza sativ

32	43	51.2	413	2 Q83SA1	Q83SA1 shigella fl
33	43	51.2	421	1 TOLA ECOLI	PI9934 escherichia
34	43	51.2	421	2 Q8FJT1	Q8FJT1 escherichia
35	43	51.2	455	2 Q91C2	Q91C2 pseudomonas
36	43	51.2	593	2 Q6AOK4	Q6AOK4 desulfofale
37	43	51.2	639	2 Q82107	Q82107 zea mays (m
38	43	51.2	707	2 Q64CP3	Q64CP3 uncultured
39	43	51.2	1924	2 Q7RSU9	Q7RSU9 giardia lam
40	42.5	50.6	189	2 Q7M495	Q7M495 homarus ame
41	42.5	50.6	189	2 Q7M496	Q7M496 homarus ame
42	42.5	50.6	300	2 Q729M4	Q729M4 desulfovibr
43	42	50.0	88	2 Q62091	Q62091 mus musculu
44	42	50.0	151	2 Q95267	Q95267 ostericgia
45	42	50.0	250	2 Q7NW09	Q7NW09 chromobacte

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	574 AA.
ID Q8SXM8			
AC Q8SXM8			
DT 01-JUN-2002 (TrEMBLrel. 21, Created)			
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE LD23509P (CG12141-PA).			
GN Name=Ats-1ys; ORFName=CG12141;			
OS Drosophila melanogaster (fruit fly).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC Ephydroidea; Drosophilidae; Drosophila.			
OX NCBI_Taxid=7227;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Berkley;			
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,			
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,			
RA Miranda A., Mungall C.J., Munoo J., Pachle J., Paragas V., Park S.,			
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,			
RA Ceiniker S.;			
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RL [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185;			
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,			
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champ M., Pfeiffer B.D.,			
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,			
RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,			
RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,			
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA de Pablos B., Delcher S., Deng Z., May A.D., Dew I., Dietz S.M.,			
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA Glodde N.A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA Harrits N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA Hestlin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,			
RA Jostali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA Mekurov G., Mishina N.V., Moberly C., Morris J., Mostrel A.,			
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pachle J.M.,			
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 CC Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 DR EMBL: AY089547; AAL90285.1; -
 DR EMBL: AF003447; AAN09255.1; -
 DR HSSP: P13030; IBBW.
 DR FlyBase; FBgn0027084; Aats-lys.
 DR GO: GO:0005737; C:cytoplasm; IEA.
 DR GO: GO:0004815; F:aspartate-CRNA ligase activity; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0004824; F:lysine-CRNA ligase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0006422; P:aspartyl-tRNA aminoacylation; IEA.
 DR GO: GO:0006430; P:lysyl-tRNA aminoacylation; IEA.
 DR GO: GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro: IPR008994; Nucleic acid OB.
 DR InterPro: IPR004364; tRNA-synt_2.
 DR InterPro: IPR003312; tRNA-synt_asep.
 DR InterPro: IPR002313; tRNA-synt_lys_2.
 DR InterPro: IPR004365; tRNA anti.
 DR InterPro: IPR006195; tRNA_ligase_II.

DR Pfam; PF00152; tRNA-synt_2; 1.
 DR Pfam; PF01336; tRNA anti. 1.
 DR PRINTS; PR01042; TRNASYNTHASP.
 DR PRINTS; PR00982; TRNASYNTHLXS.
 DR TIGRPFam; TIGR00499; lys_Dact. 1.
 DR PROSITE; PS0062; AA TRNA LIGASE II; 1.
 DR ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
 SW SEQUENCE 574 AA; 64660 MW; 861DAEA9C53EDBE CRC64;
 Query Match 60.7%; Score 51; DB 2; Length 574;
 Best Local Similarity 70.6%; Pred. No. 6.8;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 1 APEKAFKFAVKAAPAA 17
 19 ASQKAKKAKKAKKAAAPAA 35
 Db
 RESULT 2
 ID 09W327 PRELIMINARY; PRT; 607 AA.
 AC 09W327;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG12141-PB.
 GN ORFNames=CG12141;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
 RA Jitali M., Kalush F., Kapen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Morklov G., Milshina N.V., Mobarry C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Palzer K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 George R.A., Hoekins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 Svirkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 Weinstock D., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirkas R.,
 Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective."
 RT Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 Bettecourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
 Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 CC Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 DR EMBL: AEO03447; AAF46510.2; -.
 DR HSSP: P13030.1BBW.
 DR FlyBase; FBN0027084; Aars-lys.
 DR GO: GO:0005737; C:cytoplasm; IEA.
 DR GO: GO:0004815; F:aspartate-CRNA ligase activity; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0004824; F:lysine-CRNA ligase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0006432; P:aspartyl-tRNA aminoacylation; IEA.
 DR GO: GO:0006430; P:lysyl-tRNA aminoacylation; IEA.
 DR GO: GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro: IPR008994; Nucleic_acid_OB.
 DR InterPro: IPR004364; CRNA-synt_2.
 DR InterPro: IPR002312; CRNA-synt_sep.
 DR InterPro: IPR002313; CRNA-synt_lys_2.
 DR InterPro: IPR004365; CRNA-anti.
 DR InterPro: IPR006195; CRNA_ligase_II.
 DR Pfam: PF00152; CRNA-synt_2; 1.
 DR Pfam: PF01336; CRNA-anti; 1.
 DR PRINTS: PRO1042; TRNASYNTHASP.
 DR PRINTS: PRO0982; TRNASYNTHYS.
 DR TIGRFAMs: TIGR00499; LysS_bact; 1.
 DR PROSITE: PSS0862; AA TRNA LIGASE II; 1.
 DR PROSITE: PSS0862; AA TRNA LIGASE II; 1.
 KW ATP-binding; Aminoacyl-tRNA synthetase; ligase; Protein biosynthesis.
 SO SEQUENCE 607 AA; 68503 MW; 771C9870965D81B CRC64;

QY 1 APEKAEAYKAAAPA 17
 DB 52 AEQAKAEKAKAAAPA 68
 ID RLI9_AGR75 STANDARD; PRT; 179 AA.
 AC Q8UBZ5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L19.
 GN Name=PL19; OrderedLocustNames=Alt2703, AGR_C4900;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F., Jr., Woo L.,
 Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Boye D., Sr.,
 Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 Kutayavin T., Levy R., Li M.-Y., McClelland E., Palmeri A.,
 Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 Zhang S., Yoo H., Tao Y., Bidle P., Jung M., Krespan W., Perry M.,
 Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58."
 RT Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gatlung S., Miller N., Blanchard M.,
 Quirillo B., Goldman B.S., Gao Y., Askenazi M., Halling C., Mullin L.,
 Houmlet K., Gordon J., Vaudin M., Iartchouk O., Bpp A., Liu F.,
 Roullier C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 Riangan C., Crowell C., Guron J., Lomo C., Sear C., Strub G.,
 Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58."
 RT Science 294:2323-2328 (2001).
 CC -1- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
 interface and may play a role in the structure and function of the
 aminoacyl-tRNA binding site (by similarity).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L19 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL database
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AEO09216; AAL43684.1; -.
 DR EMBL: AEO08183; AAK88423.1; -.
 DR PIR: AF2908; AF2908.
 DR PIR: F97683; F97683.
 DR HAMAP: MF 00402; -; 1.
 DR InterPro: IPR001857; Ribosomal_L19.
 DR Pfam: PF01245; Ribosomal_L19; 1.
 DR PRINTS: PRO0061; Ribosomal_L19; 1.
 DR PRODOM: PD002979; Ribosomal_L19; 1.
 DR TIGRFAMs: TIGR01024; TP1S_bact; 1.
 DR PROSITE: PS01015; RIBOSOMAL_L19; 1.
 KW Complete proteome; Ribosomal protein.
 SO SEQUENCE 179 AA; 19474 MW; F3256BAA44A5AD2D1 CRC64;

Query Match 60.74; Score 51; DB 2; Length 607;
 Best Local Similarity 70.64; Pred. No. 7.2;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Query Match 54.8%; Score 46; DB 1; Length 179;
 Best Local Similarity 64.7%; Pred. No. 15;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFKFAAYKAAAPA 17
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 DB 135 ABEKARLEAKVAAQA 151

RESULT 4
 Q96M46 PRELIMINARY; PRT; 570 AA.
 ID Q96M46;
 AC Q96M46;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ32830.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 OX
 RN
 RP
 RC
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Fujimori K.,
 RA Nomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kinata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Tsujiya S., Komai F., Hara R., Takeuchi K., Arita N., Imose N.,
 RA Maeshino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Motiya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa R.,
 RA Okumura K., Nagase T., Nomura Y., Kikuchi H., Masuho Y., Yamaashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK057392; BAB71466.1; -.
 DR InterPro; IPR008938; ARM.
 SQ SEQUENCE 570 AA; 65769 MW; 65BEB6F244FC7E2 CRC64;

Query Match 54.8%; Score 46; DB 2; Length 570;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEKAFKFAAYKAAAPA 14
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 DB 194 PEKAFKFAAYKAAAPA 206
 RESULT 5
 Q81W24 PRELIMINARY; PRT; 183 AA.

AC Q81W24; Q6KX50;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=BA0013, BA50016, GBA0013;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NC NCB1_TaxID=1392;
 OX
 RN
 RP
 RC
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Risticone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA Debey R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khoult H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Niedman J.F.,
 RA Berry K.J., Flaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
 RA Salzman S.L., Thomson B., Friedlander A.W., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RT Nature 423:81-86(2003).
 RN
 RL
 RP
 RC
 RX STRAIN=Ames / isolate Porton;
 RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases."
 RT [3]
 RN
 RP
 RC
 RX STRAIN=Stierne;
 RA Hitchcock P., Jackson P., Keim P., Longstre J., Lucas S., Ohtaka R.,
 RA Richardson P., Rubin E., Rice H.;
 RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE017024; AAP24070.1; -.
 DR EMBL; AE017334; AAT29093.1; -.
 DR EMBL; AE017225; AAT52355.1; -.
 DR TIGR; BA0013;
 DR TIGR; GBA0013;
 DR Complete proteome; Hypothetical protein.
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 SQ SEQUENCE 183 AA; 20653 MW; 3BD4AC2C8D658752 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 183;
 Best Local Similarity 62.5%; Pred. No. 23;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFKFAAYKAAAPA 16
 |||:|||||
 DB 116 APEKAFKFAAYKAAAPA 131

RESULT 6
 Q8JHA3 PRELIMINARY; PRT; 244 AA.
 ID Q8JHA3;
 AC Q8JHA3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Class IV POU-domain transcription factor Brn-3.2 (fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;


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RN [1]
RP SEQUENCE FROM N.A.
RA Huvershtn J., Brose D., Bodmer D., Mullen L., Gleich O., Strutz J.,
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF526419; AAM89245.1; -.
DR HSSP; P14859; ICQT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR010982; Lambda_1like_DNA.
DR InterPro; IPR00327; POU.
DR Pfam; PF00157; POU; 1.
DR PRINTS; PRD0028; POUDOMAIN.
DR ProDom; PDD00010; Homeobox; 1.
DR ProDom; PD000583; POU; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26554 MW; 59D36AB50611BD9D CRC64;

Query Match 53.6%; Score 45; DB 2; Length 244;
Best Local Similarity 58.8%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 APEKAKEAYKAAAPA 17
Db 219 APEKRSLEAYFALQPPA 235

RESULT 7
QY 09AAC8 : PRELIMINARY; PRT; 389 AA.
AC 09AAC8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein CC0674.
GN OrderedLocustNames=CC0674;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OC NCBI_TaxID=155892;
OX
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Niernan W.C., Feldblyum T.V., Lamb M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohia N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Swinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouli H.M., Shetty J.,
RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Yamathavan J.J.,
RA Esmolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro U.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AEO05743; AAK22659.1; -.
DR PIR; G87332; G87332.
DR TIGR; CC0674; -.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000897; SRP54.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
KM Complete proteome; Hypothetical Protein.
SQ SEQUENCE 389 AA; 40769 MW; 66DD05BCEB9150E CRC64;

Query Match 53.6%; Score 45; DB 2; Length 389;
Best Local Similarity 58.8%; Pred. No. 47;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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QY 1 APEKAKEAYKAAAPA 17
Db 63 ADGKTSVETKAAAPA 79

RESULT 8
QY 085598 : PRELIMINARY; PRT; 390 AA.
AC 085598;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dihydrolysoamide succinyl transferase.
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OC NCBI_TaxID=235;
OX
RN [1]
RP SEQUENCE FROM N.A.
RA Boschiroli L., Cravero S., Rosetti O.L.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
DR EMBL; AF070932; AAC23605.1; -.
DR HSSP; P07016; 1CAT.
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolysoyllysine-residue succinyltransferase. .; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR001078; 2oxoacid_dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3 binding.
DR InterPro; IPR011053; Hybrid_motif.
DR InterPro; IPR006255; Succ.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF02817; E3 binding; 1.
DR ProDom; PD001115; 2oxoacid_dh; 1.
DR TIGRFAMs; TIGR01347; succ3_1.
KM Acyltransferase; Lipoyl; Transferase.
SQ SEQUENCE 390 AA; 41004 MW; 5A0AADB87569F5C2 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 390;
Best Local Similarity 64.7%; Pred. No. 47;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKEAYKAAAPA 17
Db 71 APEKAKEAYKAAAPA 87

RESULT 9
QY 08FYF8 : PRELIMINARY; PRT; 408 AA.
AC 08FYF8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2-oxoglutarate dehydrogenase, E2 component, dihydrolysoamide
DE succinyltransferase (EC 2.3.1.61).
GN Name=sucB; OrderedLocustNames=BR1922;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OC NCBI_TaxID=29461;
OX
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;

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RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umeyan L.A., Brinkac L.M., Beanan M.J.,
 RA Doughterty S.C., Debby R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
 RA Van Aken S.E., Riedmuller S., Tettein H., Gill S.R., White O.,
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
 RA Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
 DR EMBL: A5014482; Contains 1 lipoyl-binding domain.
 DR HSSP: P07016; 1CAT.
 DR TIGR: BR1922; -;
 DR GO: GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
 DR GO: GO:0008415; F:acyltransferase activity; IEA.
 DR GO: GO:0004149; F:diacyltransferase activity; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR GO: GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro: IPR001078; 2-oxoacid dh.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR004167; E3_binding.
 DR InterPro: IPR011053; Hybrid_motif.
 DR InterPro: IPR003016; Lipoyl_BS.
 DR InterPro: IPR006255; SucB.
 DR Pfam: PF00198; 2-oxoacid dh; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF02817; E3_binding; 1.
 DR ProDom: PD001115; 2-oxoacid dh; 1.
 DR TIGRPFAM: TIGR01347; sucB; 1.
 DR PROSITE: PS00189; LIPOYL; 1.
 KW Acyltransferase; Complete proteome; Lipoyl; Transferase.
 SQ SEQUENCE 408 AA; 42839 MW; 7EC80A61800AC64 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 408;
 Best Local Similarity 64.7%; Pred. No. 49;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPAA 17
 DB 86 AFAQKEKFAKAAAPAA 102

RESULT 10
 Q9L6H8 PRELIMINARY; PRT; 408 AA.
 AC Q9L6H8; Q7CNV5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE DIHYDROLIPONAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE
 DE DEHYDROGENASE COMPLEX (EC 2.3.1.61).
 GN Name=sucB; OrderedlocusNames=BME10141;
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M;
 RX MEDLINE=21437665; PubMed=11553602;
 RX DOI=10.1128/JAI.69.10.6537-6540.2001;
 RA Zygmunt M.S., Diaz M.A., Teixeira-Gomes A.P., Cloeckaert A.;
 RT "Cloning, nucleotide sequence, and expression of the Brucella
 RT melitensis sucB gene coding for an immunogenic dihydroliponamide
 RT succinyltransferase homologous protein.";
 RL Infect. Immun. 69:6537-6540(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;

RA Delvecchio V.G., Kapratel V., Redkar R.J., Patra G., Wujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Resnik G.,
 RA Tjalonova L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Hasekova R., Kyriades N.C., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
 DR EMBL: AF235020; AAF43701.1; -;
 DR EMBL: AE009457; AAL51323.1; -;
 DR PIR: AH3269; AH3269.
 DR HSSP: P07016; 1CAT.
 DR GO: GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
 DR GO: GO:0008415; F:acyltransferase activity; IEA.
 DR GO: GO:0004149; F:diacyltransferase activity; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR GO: GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro: IPR001078; 2-oxoacid dh.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR004167; E3_binding.
 DR InterPro: IPR011053; Hybrid_motif.
 DR InterPro: IPR003016; Lipoyl_BS.
 DR InterPro: IPR006255; SucB.
 DR Pfam: PF00198; 2-oxoacid dh; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF02817; E3_binding; 1.
 DR ProDom: PD001115; 2-oxoacid dh; 1.
 DR TIGRPFAM: TIGR01347; sucB; 1.
 DR PROSITE: PS00189; LIPOYL; 1.
 KW Acyltransferase; Complete proteome; Lipoyl; Transferase.
 SQ SEQUENCE 408 AA; 42911 MW; 16F763942B097CA7 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 408;
 Best Local Similarity 64.7%; Pred. No. 49;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAFKFAKAAAPAA 17
 DB 86 AFAQKEKFAKAAAPAA 102

RESULT 11
 Q8PGR8 PRELIMINARY; PRT; 607 AA.
 AC Q8PGR8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DIHYDROLIPONAMIDE dehydrogenase.
 GN Name=lpdA; OrderedlocusNames=XAC3659;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OC NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.F.A.,
 RA Camarotte G., Camavan F., Cardoso U., Chambergo F., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Fortighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Melandri U., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Srinioja L.A.F., Takita M.A., Tamura R.R., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Secubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 CC -1- CATALYTIC ACTIVITY: Protein N(6)-(dihydrolipoyl)lysine + NAD(+) =
 CC protein N(6)-(lipoyl)lysine + NADH.
 CC -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -1- COFACTOR: FAD (By similarity).
 CC -1- MISCELLANEOUS: The active site is a redox-active disulfide bond
 CC (By similarity).
 CC -1- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
 CC oxidoreductase family.
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
 DR EMBL; AB012016; AAM38502.1; -.
 DR HSSP; Q51235; 10JT.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR001327; FAD pyr redox.
 DR InterPro: IPR000815; Hg reductase.
 DR InterPro: IPR011053; Hybrid_motif.
 DR InterPro: IPR006258; Lipamide_dh.
 DR InterPro: IPR003016; Lipoyl_BS.
 DR InterPro: IPR000205; NAD_BS.
 DR InterPro: IPR001100; Pyr_redox.
 DR InterPro: IPR004099; Pyr_redox_dim.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR Pfam; PF02852; Pyr_redox_dim; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGRDTPASE.
 DR PRINTS; PR00411; PNDRTASE1.
 DR ProDom; PD000139; FAD_pyr_redox; 1.
 DR TIGRFAMs; TIGR01350; lipamide_dh; 1.
 DR PROSITE; PS00189; Lipoyl; 1.
 DR PROSITE; PS00076; PYRIDINE REDOX 1; 1.
 KM Complete pteridine; FAD; Flavoprotein; Lipoyl; NAD; Oxidoreductase;
 KM Redox-active center.
 SQ SEQUENCE 607 AA; 63213 MW; 2D218BCF97903D9F CRC64;
 Query Match 53.6%; Score 45; DB 2; Length 607;
 Best Local Similarity 64.7%; Pred. No. 73;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 APEKAFYAKAAPA 17
 DB 84 APEKAFYAKAAPA 100
 ID 065JG3 PRELIMINARY; PRT; 781 AA.
 AC 065JG3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE SpoIIE (DNA translocase).
 GN Name=spoIIE; ORFNames=BL01204, BL01906;
 OS Bacillus licheniformis DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 13;
 RX PubMed=15383718;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,

RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
 RT Organism with Great Industrial Potential."
 RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus
 RT licheniformis and comparisons with closely related Bacillus species."
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; AE017333; AA040801.1; -.
 DR EMBL; CP000002; AA023441.1; -.
 SQ SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;
 Query Match 53.6%; Score 45; DB 2; Length 781;
 Best Local Similarity 60.0%; Pred. No. 93;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 3 EKAKFAYAKAAPA 17
 DB 264 EKAKFAYAKAAPA 278
 ID 069Y08 PRELIMINARY; PRT; 1340 AA.
 AC 069Y08;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFp4511127 (Fragment).
 GN Name=DKFp4511127;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RG The German CDNA Consortium;
 RA Koehler K., Beyer A., Mewes
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL832376; CAH10402.1; -.
 KM Hypothetical protein.
 PT NON TER 1340 1340
 SQ SEQUENCE 1340 AA; 145772 MW; FA4635B5BE64394 CRC64;
 Query Match 53.6%; Score 45; DB 2; Length 1340;
 Best Local Similarity 64.3%; Pred. No. 1.6e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 EKAKFAYAKAAPA 16
 DB 634 ENEFEAYSPAAP 647
 ID 069Y09 PRELIMINARY; PRT; 1614 AA.
 AC 069Y09;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFp451A076 (Fragment).
 GN Name=DKFp451A076;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RG The German CDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Well B., Amid C., Oanger A.,
 RA Fob G., Han M., Wiemann S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL832347; CAH10406.1; -.
 KW Hypothetical protein.
 FT NON_TER 1614 1614
 SQ SEQUENCE 1614 AA; 175041 MW; FCE219C927BAEB9B CRC64;

Query Match 53.6%; Score 45; DB 2; Length 1614;
 Best Local Similarity 64.3%; Pred. No. 1.9e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY .3 EKAFFAYKAAAP 16
 | : ||| | |||
 Db 562 ENEFEAYSPAAP 575

RESULT 15

ID 09BEL9 PRELIMINARY; PRT; 427 AA.
 AC 09BEL9;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE M114188 protein.
 GN OrderedLocustNames=m114188;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=361;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu B., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003003; BAB50899.1; -.
 KW Complete proteome.
 SQ SEQUENCE 427 AA; 46687 MW; 8FB54C7A4F6C6676 CRC64;

Query Match 53.0%; Score 44.5; DB 2; Length 427;
 Best Local Similarity 58.8%; Pred. No. 63;
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 2 PEKAFEA-YKAAAPA 17
 | : ||| | |||
 Db 173 PQRAAFEAAYLSASAPA 189

Search completed: February 26, 2005, 23:55:46
 Job time : 75.898 secs